```
173 VVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQAI 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches 183; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LIBRARY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-08-700-607-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 1, Appli
Sequence 5, Appli
Sequence 6998, Ap
Sequence 6980, Ap
Sequence 6, Appli
Sequence 7, Appli
Sequence 8, Appli
Sequence 7290, Ap
Sequence 7290, Ap
Sequence 563, Ap
Sequence 563, Ap
Sequence 4613, Appli
Sequence 4613, Appli
Sequence 4601, Ap
Sequence 2, Appli
Sequence 2, Appli
Sequence 2, Appli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 7861, Ap
Sequence 3, Appli
Sequence 15347, A
Sequence 10562, A
                                                                                 June 23, 2005, 09:47:53 ; Search time 30.4577 Seconds (without alignments) 882.327 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                           ......VKDAMAKIQAKIPGLKRKAD 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Description
                                                                                                                                                                                                                                                                                                                                                                                                                            /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
/cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
/cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/PcTUS_COMB.pep:*
/cgn2_6/ptodata/1/iaa/PcTUS_COMB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-08-700-607-5

US-09-949-016-6998

US-09-949-016-6998

US-08-700-607-7

US-08-700-607-7

US-08-700-607-8

US-09-949-016-7290

US-09-949-016-7290

US-09-949-016-7290

US-09-149-476-563

US-09-149-476-563

US-09-149-476-411

US-09-102-540-11750

US-09-103-767-4600

US-09-103-767-4600

US-09-103-767-4600

US-09-103-767-4600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-08-899-595-3
US-09-902-540-15347
US-09-949-016-10562
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ·09-513-999C-7861
                                                                                                                                                                                                                                                                            Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                   513545 segs, 74649064 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SUMMARIES
                                                                                                                                                                                                                                                                                                                                                     Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                        - protein search, using sw model
                                                                                                                                                                                                       BLOSUM62
Gapop 10.0 , Gapext 0.1
                                                                                                                                             US-09-830-972-2-FUSED
1823
1 MEDIDQSSLVSSSTDSPPRP.
                                                                                                                                                                                                                                                                                                                                                                                                                   Issued Patents AA:*
                                                                                                                                                                                                                                                                                                            Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query
Match Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  68
92
1027
75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1255
1255
1255
1255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               262.8
262.5
262.5
262.5
262.5
262.5
262.5
262.5
262.5
261.5
261.5
                                                                                                                                                             Perfect score:
                                                                                                                                                                                                        Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  826.3
826.3
816.7
790
683
669
669
669
683
885.3
286.8
286.8
                                                        OM protein
                                                                                                                                                                             Sequence:
                                                                                                                                                                                                                                                   Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                    Database
                                                                                     Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Result
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         No.
```

```
Sequence 15, Appl
Sequence 32, Appl
Sequence 32, Appl
Sequence 2064, A
Sequence 6890, Ap
Sequence 22, Appli
Sequence 22, Appl
Sequence 22, Appl
Sequence 22, Appl
Sequence 27, Appl
                                             1142, Ap
15, Appl
15, Appl
32, Appl
                                                                                                                                                                                                                              Sequence Sequence S
                  Sequence
Sequence
Sequence
                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                         us-08-70-607-1

; Sequence 1, Application US/08700607
; Patent No. SB9700607
; Patent No. SB0700607
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; APPLICANT: Au-Young, Janice
; APPLICANT: Hillman, Jennifer L.
; TITLE OF INVENTION: TWO NOVEL HUMAN NSP-LIKE PROTEINS
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
CITY: Palo Alto
ZIP...
ZIP...
US-10-237-551-197

US-08-964-870-14

US-08-960-115-144

US-09-538-092-1142

US-09-688-1888-15

US-09-221-4170-15

US-08-221-4170-15

US-09-221-4170-15

US-09-248-796A-20654

US-09-248-796A-20654

US-09-949-016-10925

US-09-949-016-10925

US-09-949-016-10925

US-09-949-016-10925

US-09-949-016-10925

US-09-982-240-16773

US-09-9823-240A-2

US-08-9823-240-16773

US-08-9823-240-16773
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTEND Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/700,607
FILING DATE: Filed Herewith
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PF-0114 US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: BAILINGS, LLOY J.
REGISTRATION NUMBER: 36,749
REPERENCE/DOCKET NUMBER: PF-01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-85-055
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 199 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
   1318
933
933
1326
1326
1326
11326
11326
11341
11070
11089
11089
11187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linea
MOLECULE TYPE: pe
IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRANDEDNESS:
                                                            2336.2
2335.2
2335.7
2330.6
2330.4
2238.8
228.8
228.8
                                                                                                                                                                                                             228
227.4
```

ô

Gaps

ö

49.6%; Score 904; DB 2; Length 199; 97.3%; Pred. No. 1.6e-33; Live 3; Mismatches 2; Indels

Consensus

셤

ð d

셤 ð

ò

```
563 SPAATKGPGPLG-----PGAPPPLLFLNKQK-----AIDLLYWRDIKQTGIVFGSFLLL 611
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 776;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 45.3%; Score 826.3; DB Best Local Similarity 27.7%; Pred. No. 7e-29; Matches 195; Conservative 52; Mismatches 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ----LEELE-----
                   E: Incyte Pharmaceuticals, Inc.
3174 Porter Drive
                                                                                                                         MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/700,607
FILING DATE: Filed Herewith
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REGISTRATION NUMBER: PF-0114 US
TELEPHONE: 415-855-0555
                                                                                                                                                                                                                                                                                   PF-0114 US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 35 EEDEREEDERED-----DED----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ---AAAVPPAAAAPLLDFSSDSV---
                                                                                                                                                                                                                                                                                                                                                                           LENGIH: 776 amino acide
                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                              415-845-4166
                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: peptide IMMEDIATE SOURCE:
                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
      CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           101 --APERQPS----
                                                                                                                                                                                                                                                                                                                                                                                           amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                       linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 90 PRGPL----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10 VSSSTDS---
                                               Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       20 -PPP----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 307307
                                                                                                                                                                                                                                                                                                                                                                                                      STRANDEDNESS:
                                                                                            94304
                                                               STATE: C
                                                                                                                                                                                                                                                                                                                              TELEFAX:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LIBRARY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-08-700-607-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ਨੇ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              엄
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      8
                                                                                                                                                                                                                                                                                                      QKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDSLKFAVL 131
                                                                                                            MWVFTYVGALFNGLTLLILALISLFSIPVIYERHQVQIDHYLGLANKSVKDAMAKIQAKI 352
                                                                                                                              173 VVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQAI 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    74 QKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDSLKFAVL 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MWVFTYVGALFNGLTLLILALISLFSIPVIYERHQVQIDHYLGLANKSVKDAMAKIQAKI 352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           134 MWVFTYVGALFNGLTLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAKI 193
                                               QKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRLFLVDDLVDSLKFAVL 292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              233 QKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRLFLVDDLVDSLKFAVL 292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 73
                   71
14 VVDLLYWRDIKKTGVVFGASLFLLESLTVFSIVSVTAYIALALLSVTISFRIYKGVIQAI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 201;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 904; DB 4; Length 20 Pred. No. 1.6e-33; 3; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Au-Young, Janice
APPLICANT: Goli, Surya K.
APPLICANT: Hillman, Jennifer L.
ITILE OF INVENTION: TWO NOVEL HUMAN NSP-LIKE PROTEINS
NUMBER OF SEQUENCES: 9
                                                                                                                                                                                                                                                                              Sequence 9124, Application US/09949016
Patent No. 6812339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 5, Application US/08700607
Patent No. 5658708
GENERAL INFORMATION:
APPLICANT: Bandman, Olga
APPLICANT: Au-Young, Janice
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 97.3%;
Matches 183; Conservative
                                                                                                                                                                                              PGLKRKAE 199
                                                                                                                                                                         PGLKRKAD 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PGLKRKAD 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PGLKRKAE 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
ORGANISM: Human
                                                                                                                                                                                                                                               RESULT 2
US-09-949-016-9124
DS-09-949-016-9124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-949-016-9124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-08-700-607-5
                                                                                                                                                                       353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         293
                                              233
                                                                              72
                                                                                                            293
                                                                                                                                                                                                    192
                   12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 3
```

셤

ઠે

셤 ò 셤 ò g

ò

```
--WERSPAAPAPSLPPA-----AAVLPSKLPEDD----E 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    136 PPARPPPPPAGASPLAEPAAPPSTPAAPKRRGSGSSVVDLLYWRDIKKTGVVFGASLFL 195
                                                                                                                                                                                 85 VSSAMDHTFSTTSKDGEGSCYTSLISDICYPPQEDSTYFTGILQKENGHVTISESPEELG 144
                                                                                                                                                                                                                                                                                                                                                    145 TPGPSLPDVPGIESRGLFSSDSGIEMTPAESTEVNKILADPLDQMKAEÄYKYIDITRPEE 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      205 VKHQEQHHPELEDKULDFKNKDTDISIKPEGVREPDKPAPVEGKIIKDHLLEESTFAPYI 264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   265 DDLSEEQRRAPQITTPVKITLTEIEPSVETTTQEKTPEKQDICLKPSPDTVPTVTVSEPE 324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                325 DDSPGSITPPSSGTEPSAAESQGKGSISEDELITAIKEAKGLSYETAENPRPVGQLADRP 384
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 385 EVKARSGPPTIPSP-LDHEASSAESGDSEIELVSEDPMAAEDALPSGYVSFGHVGGPPS 443
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             504 VRABERAPSRRGLABPGSFLDYPSTEPQPGPELPPGDGALEPETPMLPRK-PEEDSSSNQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ----PPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -----PAAPPA-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         444 PASPSIQYSILREEREABLDSBLIIESCDASSASEESPKREQDSPPMKPSALDAIREETG
    Gaps
Indels 367;
```

g

ઠે 셤

ઠે 8 ŝ

```
RESULT 5

US-09-949-016-9180

i Sequence 9180, Application US/09949016

i Sequence 9180, Application US/09949016

i Betent No. 6812339

i GENERAL INFORMATION:

i APPLICANT: VEWTER, U. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;

FILE REFREENCE: CLOOU1307

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT FILING DATE: 2000-04-14

PRIOR APPLICATION NUMBER: 60/231,768

PRIOR PELING DATE: 2000-10-20

PRIOR PILING DATE: 2000-10-03

PRIOR PILING DATE: 2000-10-03

PRIOR PILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOOFMARE: FREESE for Windows Version 4.0

LENGTH: 439
                                                                                              VQKYSNSALGHVNSTIKELRRLFLVDDLVDSLKFAVLMWVFTYVGALFNGLTLLILALIS 315
                                                                                                                                                                                                                                                                                                                                                           PPARPPPPPPAGASPLAEPAAPPSTPAAPKRRGSGSSVVDLLYWRDIKKTGVVFGASLFL 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            83 ------APERQPS----- SDSVPPAPRGPLPAAPPA-------APERQPS----- 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            124 ELDSELIIESCDASSASEESPKREQDSPPMKPSALDAIREETGVRAEERAPSRRGLAEPG 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            108 ----WERSPAAPAPAPAPALPPA-----AAVLPSKLPEDD----EPPARPPPPPAGASPLA 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        153 EPAAPPSTPAAPKRRGSGSSVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIA 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 238 -PGAPPELFINKOK----AIDELYMRDIKQTGIVFGSFLLLEFSLTQFSVVSVVAYLA 291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        213 LALLSVTISFRIYKGVIQAIQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIK 272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              504 VRAEERAPSRRGLAEPGSFLDYPSTEPQPGPELPPGDGALEPETPMLPRK-PEEDSSSNQ 562
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            71 SGDSE-----IELVSEDPMAAEDALPSGYVSFGHVGGPPPSPASPSIQYSILREEREA 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     273 ELRRLFLVDDLVDSLKFAVLMWVFTYVGALFNGLTLLILALISLFSIPVIYERHQVQIDH 332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQAIQKSDEGHPFRAYLESEVAISEEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    184 SFLDYPSTEPQPGPELPPGDGALEPETPMLPRK-PEEDSSSNQSPAATKGPGPLG----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ----PPAFKYQFVTEPEDEEDEEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels 113;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ---AAVPPAAAAPLLDFS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 439;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  316 LFSIPVIYERHQVQIDHYLGLANKSVKDAMAKIQAKIPGLKRKAD 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  44.8%; Score 816.7; DB 4;
40.6%; Pred. No. 6.4e-29;
vative 52; Mismatches 101;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               42 EDEEEDDEDLEELEVLERKPAAGLSA----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 ED----IDQSSLVSSSTDSPPRP----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 40.6
Matches 182; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-949-016-9180
                                                                136
                                                                                                                                                                                         196
                                                                                                                                                                                                                                                                                                                      256
                                                                                                                                                                                                                                     ద
                                                            à
                                                                                                                  8
                                                                                                                                                                 8
                                                                                                                                                                                                                                                                                                                      ð
                                                                                                                                                                                                                                                                                                                                                                               셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                  ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ઠ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICAT: VENTER, J. Craig et al.

APPLICAT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
FILE REFERENCE: CLOO1307

CURRENT PAPLICATION NUMBER: US/09/949,016

CURRENT PILING DATE: 2000-04-14

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR APPLICATION NUMBER: 60/231,468

PRIOR PILING DATE: 2000-10-03

PRIOR APPLICATION NUMBER: 60/231,498

PRIOR PILING DATE: 2000-10-03

PRIOR PILING DATE: 2000-10-03

PRIOR PILING DATE: 2000-10-03

PRIOR PILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 1000-10-03

PRIOR FILING PAPEL 2000-10-03

PRIOR PILING PAPEL 2000-10-03

PRIOR FILING PAPEL 2000-10-03

PRIOR PILING PAPEL 2000-10-03

PRIOR PI
                                                                                                                                                           315
                                                                                                                                                                                            : :|: | | | |
205 VKHQEQHHPELEDKDLDFKNKDTDISIKPEGVREPDKPAPVEGKIIKDHLLEESTFAPYI 264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                85 VSSAMDHTFSTTSKDGEGSCYTSLISDICYPPQEDSTYFTGILQKENGHVTISESPEELG 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         | |:|
265 DDLSBEQRRAPQITTPVKITLTBIEPSVETTTQBKTPEKQDICLKPSPDTVPTVTVSEPE 324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EVKARSGPPTIPSP-LDHEASSAESGDSEIELVSEDPMAAEDALPSGYVSFGHVGGPPPS 443
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PASPSIQYSILREEREAELDSELIIESCDASSASEESPKREQDSPPMKPSALDAIREETG 503
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ----WERSPAAPAPSLPPA-----AAVLPSKLPEDD----E 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             145 TPGPSLPDVPGIESRGLFSSDSGIEMTPAESTEVNKILADPLDOMKAEAYKYIDITRPEE 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          325 DDSPGSITPPSSGTEPSAAESQGKGSISEDELITAIKEAKGLSYETAENPRPVGQLADRP 384
                                                         VQKYSNSALGHVNSTIKELRRLPLVDDLVDSLKPAVLMWVFTYVGALFNGLTLLILALIS :||||::
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -----AFKYQFVTEPED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ---PAAPPA----
                              LLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQAIQKSDEGHPFRAYLESEVAISEEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels 367;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
45.3%; Score 826.3; DB 4; Length 776;
Best Local Similarity 27.7%; Pred. No. 7e-29;
Matches 195; Conservative 52; Mismatches 91; Indels 367
                                                                                                                                                                                                                                                                                 316 LFSIPVIYERHQVQIDHYLGLANKSVKDAMAKIQAKIPGLKRKAD 360
                                                                                                                                                                                                                                                                                                                      -------EEFIE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 6998, Application US/09949016
Patent No. 6812339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ---AAAVPPAAAAPLLDFSSDSV---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRGPL-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -----ddd-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       --APEROPS---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10 VSSSTDS----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  , ORGANISM: Human
US-09-949-016-6998
                          196
                                                                                                                                                    256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          385
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          99
```

g

ઠ

ઠે

g

ઠે

g

ઠે g ò

ઠે

g

ઠે

δ

```
231 AIQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRLFLVDDLVDSLKFA 290
                       260 SNSALGHVNSTIKELRRLFLVDDLVDSLKFAVLMWVFTYVGALFNGLTLLILALISLFSI 319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             200 TVFSIVSVTAYIALALLSVTISFRIYKGVIQAIQKSDEGHPFRAYLESEVAISEELVQKY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         171 SSVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           291 VLAWVFTYVGALFNGLTLLILALISLFSIPVIYERHQVQIDHYLGLANKSVKDAMAKIQA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               37.5%; Score 683; DB 2; Length 208; 67.4%; Pred. No. 1.8e-23;
                                                                                                                                                                                                                                                                                                                                    APPLICANT: Bandman, Olga
APPLICANT: Au-Young, Janice
APPLICANT: Goli, Surya K.
APPLICANT: Hillman, Jennifer L.
TITLE OF INVENTION: TWO NOVEL HUMAN NSP-LIKE PROTEINS
NUMBER OP SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
                                                                                                                                                                          ||:| :|| || || || || 316 PVVYVKHQAQIDQYLGLVRTHINAVVAKIQAKIPGAKRHAE 356
                                                                                                                                                      PVIYERHQVQIDHYLGLANKSVKDAMAKIQAKIPGLKRKAD 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: FastSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/700,607
FILING DATE: Filed Herewith
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0114 US
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                   Sequence 7, Application US/08700607
Patent No. 5858708
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEPHONE: 415-855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         208 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 208 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear
MOLECULE TYPE: peptide
IMMEDIATE SOURCE:
LIBRARY: GenBank
CLONE: 307311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity 67.4
Matches 128; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OPERATING SYSTEM: DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: amino acid
STRANDEDNESS: si
                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          u.s.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZIP: 94304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STATE: C. COUNTRY:
                                                                                                                                                                                                                                                                       US-08-700-607-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-08-700-607-7
                                                                                                                                                      320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        셤
                                                                                                            a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ઠે
                               g
                                                                     ઠે
                                                                                                                                                      ઠે
                                                                                                                                                                                      셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -LAEPGSFLDYPSTEPQ------PGPELPPGDGALEPETPMLPRK-PEEDSSSNQSPAA 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  95 PAAPPAA----PERQPSWERSPAAPAPSLPPA-----AAVLPSKLPEDD----EPPAR 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              140 PPPPPPAGASPLAEPAAPPSTPAAPKRRGSGSSVVDLLYWRDIKKTGVVFGASLFLLLSL
199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4 EDALPSGYVSFGHVGGPPPSPASPSIQYSILREEREAELDSELIIESCDASSASEESPKR 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             64 EODS-----DAIREETGVRAEERAPSRĞ-- 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              --EEEDEE 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EDDEDLEELEVLERKPAAGLSAAAVPPAAAPLLDFSSDSV------PPAPRGPL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            90;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 2; Length 356;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                           GENERAL INFORMATION:

APPLICANT: Bandman, Olga
APPLICANT: Bridman, Olga
APPLICANT: Goli, Surya K.
APPLICANT: Hillman, Jennifer L.
IITLE OF INVENTION: TWO NOVEL HUMAN NSP-LIKE PROTEINS
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaccuticals, Inc.
STREET: 3174 Porter Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 EDIDQSSLVS-SSTDSPPRPP--PAFKYQFVTEPEDEE-DEE-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          87;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    43.3%; Score 790; DB 2 44.1%; Pred. No. 7e-28;
                                                                                                                                                                                                                                                                                                                                                                                            ATTACHES.

STREET: 3174 Porter Drive
CITY: Palo Alto
CITY: Palo Alto
CUNTRE: U.S.
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OMPERATING SYSTEM: DOS
SOFTWARE: FeatSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/700,607
FILING DATE: Filed Herewith
ATTORNEY/AGENT INFORMATION:
NAMME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REGISTRATION NUMBER: PF-0114 US
TELEPRONE 415-855-0555
TELEPRONE 415-855-0555
TELEPRONE 415-855-0155
TELEPRONE SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 356 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          47; Mismatches
                                                           333 YLGLANKSVKDAMAKIQAKIPGLKRKAD 360
                                                                                   Sequence 6, Application US/08700607
Patent No. 5858708
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 356 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 43.3
Best Local Similarity 44.1
Matches 177; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IMMEDIATE SOURCE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LIBRARY: General Street 307309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: li
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0-409-004-80
08-08-100-601-6
                                                                                                                                                      RESULT 6
US-08-700-607-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   원
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ઠે
                     유
                                                                                             셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ઠ
                                                           ò
```

```
Sequence 8859, Application US/09949016

Fatent No. 681239
GENERAL INFORMATION:
GENERAL INFORMATION:
FAULCANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CLOO1307
CURRENT APPLICATION NUMBER: 60/241,755
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-00-03
PRIOR PILING DATE: 2000-00-03
PRIOR FILING DATE: 2000-00-08
PRIOR FILING DATE: 2000-00-08
SOFTWARE: FASISEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-949-016-7290

Sequence 7290, Application US/09949016

Patent No. 6812133

GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

CURRENT PILICATION NUMBER: US/09/949,016

CURRENT FILING DATE: 2000-04-14

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-01-03

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             232 IOKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRLFLVDDLVDSLKFAV 291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       123 FWHLMTYVGAVFNGITLLILAELLIFSVPIVYEKYKTQIDHYVGIARDQTKSIVEKIQAK 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3 SVHDLIFWRDVKKTGFVFGTTLIMLLSLAAFSVISVVSYLILALLSVTISFRIYKSVIQA 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      292 LMWVFTYVGALFNGLTLLILALISLFSIPVIYERHQVQIDHYLGLANKSVKDAMAKIQAK 351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    172 SVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 192;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        35; Indela
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; Score 625.9; DB 4; Pred. No. 5.9e-21; 40; Mismatches 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           34.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 60.0
Matches 114; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 352 IPGL-KRKAD 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              :||: |:||:
183 LPGIAKKKAE 192
US-09-949-016-8859
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-949-016-8859
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           JS-09-949-016-7290
                                                                                                                                                                                                                                                                                                                                                                                                                    SEQ ID NO 8859
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQ ID NO 7290
LENGTH: 588
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                171 SSVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQ 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         231 AIQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRLFLVDDLVDSLKFA 290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 291 VLMWVFTYVGALFNGLTLLILALISLFSIPVIYERHQVQIDHYLGLANKSVKDAMAKIQA 350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10 SQAIDLLYWRDIKQTGIVFGSFLLLFSLTQFSVVSVVAYLALAALSATISFRIYKSVLQ 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                 APPLICANT: Bandman, Olga
APPLICANT: Au-Young, Janice
APPLICANT: Au-Young, Janice
APPLICANT: Goli, Surya K.
APPLICANT: Hillman, Jennifer L.
TITLE OF INVENTION: TWO NOVEL HUMAN NSP-LIKE PROTEINS
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; DB 2; Length 267;
1.2e-22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  36.7%; Score 669; DB illarity 66.7%; Pred. No. 1.2e-Conservative 32; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READBLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FRAESEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION DATE:
APPLICATION UNMER: US/08/700,607
ATTORNEY, AAGNT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: 36,749
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                          Sequence 8, Application US/08700607
Patent No. 5858708
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     267 amino acids amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS
                351 KIPGLKRKAD 360
                                                            199 KIPGAKRHÁE 208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
Matches 124; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                351 KIPGLK 356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KIPGAR 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDIAL
LIBRARY: Gear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           u.s.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: amino a STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY: U
ZIP: 94304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-08-700-607-8
                                                         유
                ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ઠ
```

Indels 237;

Length 588;

; Score 585.3; DB 4; ; Pred. No. 3.4e-18; 52; Mismatches 117;

Query Match 32.1 Best Local Similarity 27.5 Matches 154; Conservative

RESULT

ð

```
R APPLICATION NUMBER: 60/047,615
R FILING DATE: 1997-05-23
R APPLICATION NUMBER: 60/047,597
R PILING DATE: 1997-05-23
R APPLICATION NUMBER: 60/047,502
R PILING DATE: 1997-05-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 563, Application US/09149476 Patent No. 6420526
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           [LING DATE: 1997-03-07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1997-03-0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1997-03-07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ERXAATOSHSISSSSF---
                                                                                                         241 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 44.44
Matches 111; Conservative
TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS
                                                                                                                                                                  single
                                                                                                                                                                                           TOPOLOGY: linear MOLECULE TYPE: peptide IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        204 PSKTPWNRQK 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              349 QAKIPGLKRK 358
                                                                                                                                                                                                                                                                                  LIBRARY: THPINOB01
CLONE: 31870
                                                                                                                                                                                        linear
                                                                                                                               TYPE: amino acid
STRANDEDNESS: si
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE:
                                                                                                     LENGTH:
                                                                                                                                                                                                                                                                                                                                                 US-08-700-607-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BARLIER PARLIER PARLIE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EARLIER
EARLIER
EARLIER
EARLIER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ठ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     95 PAAPPAAPER------PPAAVLPSK-- 129
                                                                                                                                                                                                                                                                                                                                                                                                                                       212 EDEBPQEPNKLETGEAGEBLDLRLRLAQPS---SPEVLTPQLSPGSGTPQAGTPSPSRSR 268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      329 VYKTVPILELSPPLWTAIGWVQRGPTPPTPVLRVLLKWAKSPRSSGVPSLSLGADMGSKV 388
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         389 ADLLYWKDTRISGVVFTGLMVSLLCLLHFSIVSVAAHLALLLLCGTISLRVYRKVLQAVH 448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -----TEGGNDDSDFRELHTAREFSEEDEETTSQDWGTPREL 105
                                                                                                                                                                                           106 TFSYIAFDGVVGSGGRRDSTARRPRPQGRSVSEPRDQHPQPSLGDSLESIPSLSQSPEPG 165
                                                                                                                                                                                                                                                                                                                     ---DPDTAPPSERPLEDLRLRLDHLGWVARGTGSGEDSSTSSSTPL 211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                269 DSNSGPEEPLLEEEEKQWGPLEREPVRGQCLDSTDQLEFTVEPRLLGTAMEWLKTSLLLA 328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ----PLAEPAAP-----SGSSV 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   174 VDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQAIQ 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KSDEGHPFRAYLESEVAISEELVOKYSNSALGHVNSTIKELRRLFLVDDLVDSLKFAVLM 293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WVFTYVGALFNGLTLLILALISLFSIPVIYERHQVQIDHYLGLANKSVKDAMAKIQAKIP 353
            ---- 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ---PPPPAGAS---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Bandman, Olga
APPLICANT: Bandman, Olga
APPLICANT: Au-Young, Janice
APPLICANT: Goll, Surya K.
APPLICANT: Goll, Surya K.
APPLICANT: Hillman, Jennifer L.
TITLE OF INVENTION: TWO NOVEL HUMAN NSP-LIKE PROTEINS
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incvr. N.
STREET CONTROLLES NOVEL HUMAN NSP-LIKE PROTEINS
CORRESPONDENCE ADDRESS:
         SLVSSSTDSPPRPPAFKYQFVTE-PEDEED--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: Filed Herewith ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0114 US
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE: Diskette
COMPUTER: IBM COMPATED:
CORRATING SYSTEM: DOS
SOFTWARE: FASTSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/700,607
FILING DATE: Filed Herewith
                                                                                                                                                                                                                                                        65 LSAAAVPPAAAAPLLDFSSDSVPPAPR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -----PPARPP-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GL-----KRKAD 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 569 GTGALASAAAAVSGSKAKAE 588
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 3, Application US/08700607
Patent No. 5858708
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STREET: 3174 Porter Drive CITY: Palo Alto STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ZIP: 94304
COMPUTER READABLE FORM:
                                                                      59 STASSTPDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        u.s.
                                                                                                                                                                                                                                                                                                                     166 RRG--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-08-700-607-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  294
                                                                                                                                                                                                                                                                                                                                                                                                                                       셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           요
                                                                                                                                                                                        요
                                                                                                                                                                                                                                                                                                              g
                                                                                                                                                                                                                                                                                                                                                                              ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           à
                                                                                                                                  à
```

```
109 ERSPAAPAPSLPPAAAVLPSKLPEDDEPPARPPPPPPAGASPLAEPAAPPSTPAAPKRG 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           44 SSCAVHDLIXWRDVKKTGFVFGTTLIMLELARAFSVISVVSYLILALLSVTISFRIYKSV 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IQAIQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRLFLVDDLVDSLK 288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          289 FAVLMWVFTYVGALFNGLTLLILALISLFSIPVIYERHQVQIDHYLGLANKSVKDAMAKI 348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ---KV 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                  ---GAEPSAPGGGGSPGACPA----LGTKSCS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SGSSVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGV
                                                                                                                                                           Gaps
                                                                                                                                                   39;
               Length 241;
                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         164 LAVFMWLMTYVGAVFNGITLLILAELLIXSVPIVYXKY---
30.1%; Score 548.1; DB 2;
44.4%; Pred. No. 3e-17;
ive 40; Mismatches 60;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Rosen et al.
TITLE OF INVENTION: 186 Human Secreted proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EARLIER APPLICATION NUMBER: 007/0598/04493
EARLIER FILING DATE: 1998-03-06
EARLIER FILING DATE: 1997-03-07
EARLIER FILING DATE: 1997-03-07
EARLIER FILING DATE: 1997-03-07
EARLIER FILING DATE: 1997-03-07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION NUMBER: US/09/149,476
CURRENT FILING DATE: 1998-09-08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: 60/047,600
APPLICATION NUMBER: 60/047,600
THE PROPERTY OF 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: 1997-03-07
APPLICATION NUMBER: 60/040,336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: 1997-03-07
APPLICATION NUMBER: 60/040,334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: 60/040,163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: 60/038,621
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: 60/040,626
```

NUMBER: 60/047,633 1997-05-23 NUMBER: 60/047,583 1997-05-23 NUMBER: 60/047,617 1997-05-23 NUMBER: 60/047,618 1997-05-23 NUMBER: 60/047,503 1997-05-23 NUMBER: 60/047,592 NUMBER: 60/047,592 1997-05-23 NUMBER: 60/047,592 1997-05-23 NUMBER: 60/047,592	NUMBER: 60/047,50 1997-05-23 NUMBER: 60/047,59 11997-05-23 NUMBER: 60/047,59 1997-05-23 NUMBER: 60/047,59 1997-05-23 NUMBER: 60/047,59 1997-05-23 NUMBER: 60/047,59 1997-05-23 NUMBER: 60/047,63 1997-05-23 NUMBER: 60/047,63 1997-05-23 NUMBER: 60/047,63 1997-05-23 NUMBER: 60/047,63 1997-05-23 NUMBER: 60/047,63 1997-05-23 NUMBER: 60/047,63 1997-05-23 NUMBER: 60/047,60 1997-05-23 NUMBER: 60/047,60 1997-04-11	NUMBER: 60/043,569 1997-04-11 NUMBER: 60/043,311 NUMBER: 60/043,671 1997-04-11 NUMBER: 60/043,674 1997-04-11 NUMBER: 60/043,669 1997-04-11 NUMBER: 60/043,312 1997-04-11 NUMBER: 60/043,313 1997-04-11 NUMBER: 60/043,313 1997-04-11 NUMBER: 60/043,313 1997-04-11 NUMBER: 60/043,315 1997-04-11 NUMBER: 60/048,974 1997-04-11 NUMBER: 60/048,974 1997-04-12 NUMBER: 60/056,886 1997-08-22 NUMBER: 60/056,893
TION PATE PATE PATE PION PATE PION PATE PION PATE PION PATE PION PATE PION PATE PION PATE PION PATE PION PATE PION PATE PION PION PION PION PION PION PION PION		APPLICATION TELLING DATE: APPLICATION FILING D
EARLIER BARLIER BARLIER	EARLIER	BARLIER

BEALLIER FILING DATE: 1997-08-25

BEALIER FILING DATE: 1997-08-27

BEALIER FILING DATE: 1997-08-27

BEALIER FILING DATE: 1997-08-27

BEALIER FILING DATE: 1997-08-22

BEALIER PILING DATE: 1997-08-22

BEALIER FILING DATE: 1997-08-23

BEALIER PILING DATE: 1997-08-23

us-09-830-972-2-fused.rai

```
FILING DATE: 1997-05-23
APPLICATION NUMBER: 60/047,615
APPLICATION DATE: 1997-05-23
APPLICATION NUMBER: 60/047,597
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: 1997-03-07
APPLICATION NUMBER: 60/047,600
                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQ ID NOS: 36681
SOFTWARE: Patent.pm
SEQ ID NO 6304
LENGTH: 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              60; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 PAAGLSAAAV 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              59 PAAGLSAAPV 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-513-999C-6304
                         346 AKIQAKIP 353
                                                                196 DKİRVAİP 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILE REFERENCE: PZ002P1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
Matches 60; Conserv
                                                                                                                                                   US-09-513-999C-6304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-149-476-411
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EARLIER 1
EARLIER 1
EARLIER 1
EARLIER 1
EARLIER 1
                                                       g
                         à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ద
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 AFHNYMNAAMVHINRALKLIRLFLVBDLVDSLKLAVFMWLMTYVGAVFNGITLLILAEL 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                76 KSVTQAVQKTNEGHPFKDYLELDLTLSHEKVQNIAGVAVAHINGFISELRRLFLVEDIID 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 195 LLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQAIQKSDEGHPFRAYLESEVAISEE 254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         166 RRGSGSSVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIY 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         226 KGVIQAIQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRLFLVDDLVD 285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        286 SLKFAVLMWVFTYVGALFNGLTLLILALISLFSIPVIYERHQVQIDHYLGLANKSVKDAM 345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                255 LVQKYSNSALGHVNSTIKELRRLFLVDDLVDSLKFAVLMWVFTYVGALFNGLTLLILALI 314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      16 RKMSNRLLESLIYWRDVKKSGIVFGAGLITLAAISSFSVISVFAYLSLLTLFGTVAFRIY 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 45:13. Application US/09270767
Patent No. 6703491
GENERAL INFORMATION:
APPLICANT: Homburger et al.
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster FILE REFERENCE: File Reference: 7326-094
CURRENT FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62517
SOFTWARE: PatentIn Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
29.6%; Score 539.9; DB 4; Length 168;
Best Local Similarity 59.3%; Pred. No. 3.6e-17;
Matches 99; Conservative 36; Mismatches 31; Indels 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               315 SLFSIPVIYERHQVQIDHYLGLANKSVKDAMAKIQAKIPGL-KRKAD 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 28.6%; Score 522; DB 4; Length 219; Best Local Similarity 50.5%; Pred. No. 3.8e-16; Matches 95; Conservative 43; Mismatches 50; Indels
                                                                                                                                                                                                                                                                                        R APPLICATION NUMBER: 60/056, 884
R FILING DATE: 1997-08-22
R FILING DATE: 1997-09-05
R PILING DATE: 1997-09-05
R APPLICATION NUMBER: 60/049, 610
R APPLICATION NUMBER: 60/061, 060
R APPLICATION NUMBER: 60/061, 060
R FILING DATE: 1997-06-13
R APPLICATION NUMBER: 60/056,909
R FILING DATE: 1997-08-22
R APPLICATION NUMBER: 60/056,875
R APPLICATION NUMBER: 60/056,862
R APPLICATION NUMBER: 60/056,862
R FILING DATE: 1997-08-22
R APPLICATION NUMBER: 60/056,887
R RAPLICATION NUMBER: 60/056,908
R FILING DATE: 1997-08-22
R APPLICATION NUMBER: 60/056,908
R FILING DATE: 1997-08-22
                                                                                                                                                                                                                                                   APPLICATION NUMBER: 60/057,650
FILING DATE: 1997-09-05
                                                                                                                                                                                                           APPLICATION NUMBER: 60/048,964
FILING DATE: 1997-06-06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Drosophila melanogaster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 13
US-09-270-767-45132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-270-767-45132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQ ID NO 45132
LENGTH: 219
                                                             EARLIER I
EARLIER I
EARLIER I
                                                                                                                                                                                                                                                                                                                                                                                            EARLIER F
EARLIER P
EARLIER F
                                                                                                                                               EARLIER I
EARLIER I
EARLIER I
                                                                                                                                                                                                           EARLIER 1
EARLIER 1
EARLIER 1
                                                                                                                                                                                                                                                                                                                                                        EARLIER |
                                                                                                                                                                                                                                                                                                               EARLIER
EARLIER
                                                                                                                                                                                                                                                                                            EARLIER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                유
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 à
```

```
1 MEDIDOSSLVSSSTDSPPRPPARKYQFVTEPEDEEDEEBEEDEEEDBELEVLERK
Sequence 6304, Application US/09513999C
Patent No. 6783961
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Duclert, A.
APPLICANT: Giordano, J.Y.
TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
Patent No. 6783961
FILE REFERENCE: 59.US2.REG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ;
;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 286.8; DB 4; Length 68;
Pred. No. 1.9e-06;
4; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: 186 Human Secreted proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRENT FILING DATE: 1998-09-08
EARLIER APPLICATION NUMBER: PCT/US98/04493
EARLIER FILING DATE: 1998-03-06
EARLIER FILING DATE: 1998-03-06
EARLIER FILING DATE: 1997-03-07
EARLIER FILING DATE: 1997-03-07
EARLIER FILING DATE: 1997-03-07
EARLIER FILING DATE: 1997-03-07
EARLIER FILING DATE: 1997-03-07
EARLIER APPLICATION NUMBER: 60/040,626
EARLIER APPLICATION NUMBER: 60/040,626
EARLIER APPLICATION NUMBER: 60/040,334
EARLIER FILING DATE: 1997-03-07
EARLIER FILING DATE: 1997-03-07
EARLIER FILING DATE: 1997-03-07
EARLIER FILING DATE: 1997-03-07
EARLIER FILING DATE: 1997-03-07
EARLIER FILING DATE: 1997-03-07
EARLIER FILING DATE: 1997-03-07
EARLIER FILING DATE: 1997-03-07
EARLIER FILING DATE: 1997-03-07
EARLIER APPLICATION NUMBER: 60/040,336
EARLIER APPLICATION NUMBER: 60/040,163
                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/09/513,999C
CURRENT FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/122,487
PRIOR FILING DATE: 1999-02-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION NUMBER: US/09/149,476
CURRENT FILING DATE: 1998-09-08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 411, Application US/09149476
Patent No. 6420526
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15.7%;
85.7%;
```

·			
1997-05- NUMBER: 6 1997-05- NUMBER: 6 1997-05- NUMBER: 6 1997-05- NUMBER: 6 1997-05- NUMBER: 6 1997-05- NUMBER: 6 1997-05- NUMBER: 6 NUMBER: 6	5-23 60/047, 5-23 60/047, 5-23 60/047, 5-23 60/047, 5-23 60/047, 5-23 60/047, 5-23 60/047, 5-23 60/047,	$\begin{array}{cccccccccccccccccccccccccccccccccccc$	MBER: 60 997-08-2 997-08-2 997-08-2 MBER: 60 997-08-2 997-08-2
DATE DATE DATE DATE DATE DATE DATE DATE	APPLICATION FILLING DATE: FILLING DATE: APPLICATION FILLING DATE: FILL	DATE DATE	ATION DATE: DATE: DATE: ATION DATE: ATION
EARLIER EARLIER	EARLIER EAR	EARLIER EAR	EARLIER EARLIER EARLIER EARLIER EARLIER EARLIER EARLIER EARLIER

RARLIER APPLICATION NUMBER: 60/056,630
RARLIER APPLICATION NUMBER: 60/056,662
RARLIER PILING DATE: 1997-08-22
RARLIER PILING DATE: 1997-08-22
RARLIER FILING DATE: 1997-08-22
RARLIER PILING DATE: 1997-08-23
RARLIER PILING DATE: 1997-08-23
RARLIER PILING DATE: 1997-08-23
RARLIER PILING DATE: 1997-08-23
RARLIER PILING DATE: 1997-08-23
RARLIER PILING DATE: 1997-08-23
RARLIER PRILING DATE: 1997-08-23
RARLIER PILING DATE: 1997-08-23
RARLIER PRILING DATE: 1997-08-23
RARLIER PILING DATE: 1997-08-23
RARLIER PRILING DATE: 1997-08-23
RARLIER PRILING DATE: 1997-08-23
RARLIER PRILING DATE: 1997-08-23
RARLIER PRELICATION NUMBER: 60/047, 508
RARLIER PRELICATION NUMBER:

Search completed: June 23, 2005, 10:17:47 Job time: 32.4577 secs

```
June 23, 2005, 09:56:59; Search time 108.849 Seconds (without alignments) 1271.831 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                  US-09-830-972-2-FUSED
1823
1 MEDIDQSSLVSSSTDSPPRP......VKDAMAKIQAKIPGLKRKAD 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Published Applications AA:*

1: /cgn2_6/ptodata/1/pubpaa/USO7_PUBCOMB.pep:*
2: /cgn2_6/ptodata/1/pubpaa/PCT NEW PUB.pep:*
3: /cgn2_6/ptodata/1/pubpaa/PCT NEW PUB.pep:*
4: /cgn2_6/ptodata/1/pubpaa/USO6_NEM PUB.pep:*
5: /cgn2_6/ptodata/1/pubpaa/USO6_PUBCOMB.pep:*
6: /cgn2_6/ptodata/1/pubpaa/USO8_NEW PUB.pep:*
7: /cgn2_6/ptodata/1/pubpaa/USO8_NEW PUB.pep:*
8: /cgn2_6/ptodata/1/pubpaa/USO8_NEW PUB.pep:*
9: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*
11: /cgn2_6/ptodata/1/pubpaa/USO9_PUBCOMB.pep:*
11: /cgn2_6/ptodata/1/pubpaa/USO9_PUBCOMB.pep:*
11: /cgn2_6/ptodata/1/pubpaa/USO9_NEW PUB.pep:*
13: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*
14: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*
15: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*
16: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*
17: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*
18: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*
19: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*
19: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*
21: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*
22: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1717557 segs, 384547976 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                          OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                      BLOSUM62
Gapop 10.0 , Gapext 0.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                                                                                                                                                                                                                                                                        Title:
Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                         Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Database
                                                                                                                                                                                           Run on:
```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	(-20 Sequence 20, Appl	===			-10 Sequence 10, Appl				6 Seguence 6, Appli	
SUMMARIES	ID	9 US-09-893-348-20	US-10-810-653	US-10-205-194-164	US-09-893-348-18	US-10-810-653	US-10-633-423-10	US-10-427-741	US-10-267-502	US-09-789-386-	US-09-765-205-6	0 6 6 6 6 6 6 6 7 1
	08	6	16	14	σ	16	16	16	15	6	0	d
	Match Length DB	360	360	379	1163	1163	1162	1162	1163	373	373	273
ا ع مد	Match	7.66	7.66	99.2	95.0	95.0	89.8	89.8	89.0	87.9	87.9	0 20
	Score	1817	1817	1808.1	1732.7	1732.7	1637	1637	1622.9	1603.3	1603.3	1603
1	No.	-	7	e	4	2	9	7	80	0	10	=

കകകക	4 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7	Sequence 9, Appli Sequence 23, Appli Sequence 7, Appli Sequence 7, Appli Sequence 21, Appli Sequence 21, Appli	25,129,417	0 4 1 4 0 0 0 4 1 4 0 0 0 0 0 0 0 0 0 0
4.00000	US-09-758-140- US-09-893-140- US-09-893-140- US-10-060-036 US-10-267-502	16 US-10-327-213-9 16 US-10-466-258-9 16 US-10-810-653-23 15 US-10-408-967-7 9 US-09-893-348-21 16 US-10-810-653-21		15 US-10-267-502-430 16 US-10-723-860-1481 14 US-10-267-502-432 15 US-10-267-502-432 15 US-10-267-502-432 15 US-10-660-946-6 15 US-10-660-946-7 15 US-10-276-774-2330 14 US-10-106-698-6222 14 US-10-205-194-127
373 373 373 373	1192	1192 1192 1192 1192 199	1000 1000 1000 1000 1000	2003 2003 2003 2003 2003 2003
87.9 87.9 87.9 87.9		8 8 8 8 9 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 4 4 4 4 4 4 4 4 6 6 6 6 6 6 6 6 6 6 6	.44446666 10004467766 1000467766
1603.3 1603.3 1603.3 1603.3	1518.4 1518.4 1518.4 1518.4	1518.4 1518.4 1518.4 1511.4 921	9004 9004 9004 895 895 866 3	1 00000 P
12 13 15 16	22 20 20 20 20 20 20 20 20	2 2 2 2 2 2 4 3 4 4 4 4 4 4 4 4 4 4 4 4	9 9 9 9 9 9 6 9 6 9 6 9 9 9 9 9 9 9 9 9	3 3 3 3 3 4 4 4 4 4 4 4 5 5 4 5 5 6 5 6 6 6 6 6 6

ALIGNMENTS

```
APPLICANT: COHEN, ITUN R.

APPLICANT: BESERMAN, Pierre
APPLICANT: BESERMAN, Pierre
APPLICANT: MOSONEGO, Alon
APPLICANT: MOSONEGO, Alon
APPLICANT: MOSONEGO, Alon
APPLICANT: MOSONEGO, Alon
APPLICANT: MOSONEGO, Alon
FILE REFERENCE: EIS-SCHWART-2-2A
FILE REFERENCE: EIS-SCHWART-2-2A
CURRENT PLING DATE: 2001-06-28
FILE REPERICATION NUMBER: US 09/314,161
FRIOR FILING DATE: 1999-05-19
FRIOR FILING DATE: 1998-12-22
FRIOR FILING DATE: 1998-07-21
FRIOR FILING DATE: 1998-07-21
FRIOR FILING DATE: 1998-07-21
FRIOR FILING DATE: 1998-07-21
FRIOR FILING DATE: 1998-07-21
FRIOR FILING DATE: 1998-07-21
FRIOR FILING DATE: 1998-07-21
FRIOR FILING DATE: 1998-07-21
FRIOR FILING DATE: 1998-07-21
FRIOR FILING DATE: 1998-07-21
FRIOR FILING DATE: 1998-07-21
FRIOR FILING DATE: 1998-07-21
FRIOR FILING DATE: 1998-07-21
FRIOR FILING DATE: 1998-07-21
FRIOR FILING DATE: 1998-07-21
FRIOR FILING DATE: 1998-07-21
FRIOR FILING DATE: 1998-07-21
FRIOR FILING DATE: 1998-07-21
FRIOR FILING DATE: 1998-07-21
FRIOR FILING DATE: 1998-07-21
FRIOR FILING DATE: 1998-07-21
FRIOR FILING DATE: 1998-07-21
FRIOR FILING DATE: 1998-07-21
FRIOR FILING DATE: 1998-07-21
FRIOR FILING DATE: 1998-07-21
FRIOR FILING DATE: 1998-07-21
FRIOR FILING DATE: 1998-07-21
FRIOR FILING DATE: 1998-07-21
FRIOR FILING DATE: 1998-07-21
FRIOR FILING DATE: 1998-07-21
FRIOR FILING DATE: 1998-07-21
FRIOR FILING DATE: 1998-07-21
FRIOR FILING DATE: 1998-07-21
FRIOR FILING DATE: 1998-07-21
FRIOR FILING DATE: 1998-07-21
FRIOR FILING DATE: 1998-07-21
FRIOR FILING DATE: 1998-07-21
FRIOR FILING DATE: 1998-07-21
FRIOR FILING DATE: 1998-07-21
FRIOR FILING DATE: 1998-07-21
FRIOR FILING DATE: 1998-07-21
FRIOR FILING DATE: 1998-07-21
FRIOR FILING DATE: 1998-07-21
FRIOR FILING DATE: 1998-07-21
FRIOR FILING DATE: 1998-07-21
FRIOR FILING DATE: 1998-07-21
FRIOR FILING DATE: 1998-07-21
FRIOR FILING DATE: 1998-07-21
FRIOR FILING DATE: 1998-07-21
FRIOR FILING DATE: 1998-07-21
FRIOR FRIOR FRIOR DATE: 1998-07-21
FRIOR FRIOR FRIOR DATE: 1998-07-21
FRIOR FRIOR FRIOR DATE: 1998-07-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 360;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 99.7%; Score 1817; DB 9; Best Local Similarity 99.7%; Pred. No. 8.9e-55; Matches 359; Conservative 0; Mismatches 1;
                                                                                                                                                                 GENERAL INFORMATION:
APPLICANT: EISENBACH-SCHWARTZ, Michal
APPLICANT: COHEN, Irun R.
                                                 ; Sequence 20, Application US/09893348
; Patent No. US20020072493A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; ORGANISM: Rattus norvegicus
US-09-893-348-20
US-09-893-348-20
```

ö

Gaps

ö

1; Indels

Company Comp	RESULT 3 RESULT 3 Sequence 164, Application US/10205194 Sequence 164, Application US/10205194 Sequence 164, Application No. US20030134301Al Septembert Company APPLICANT: Warner-Lambert Company APPLICANT: Lee, Kevin APPLICANT: Brooksbank, Robert APPLICANT: Pinnock, Alistair APPLICANT: Pinnock, Robert APPLICANT: Pinnock, Robert APPLICANT: Pinnock, Robert APPLICANT: Pinnock Robert APPLICANT: Identification and Use of Molecules Implicated in APPLICANT: Identification and Use of Molecules Implicated in	AND THEIR USE	Query Match Best Local S Matches 359 Qy 1 Db 1	61 61 121 121 171	0; Qy 222 PRIYKGVIQ 60 Db 241 PRIYKGVIQ 60 Qy 282 DLVDSLKFA 120 Db 301 DLVDSLKFA 1120 Qy 342 XDAMAKIQA 1180 Db 361 KDAMAKIQA
MEDIDQSSLVSSSTDSPRPPPAFKYQFVTEPEDEEDEEDEEDEEDEELEVLERK	Qy 181 DIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQALQKSDEGHP Db 181 DIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQALQKSDEGHP Db 241 FRAYLESEVALSEELVQKYSNSALGHVNSTIKELRELVDDLVDSLKFAVLMWVFTYVG Db 241 FRAYLESEVALSEELVQKYSNSALGHVNSTIKELRELVDDLVDSLKFAVLMWVFTYVG QQ 301 ALFNGLTLLIALISLFSIPVIYERHQVQIDHYLGLANKSVKDAMAKIQAKIPGLKRAD Db 301 ALFNGLTLLIALISLFSIPVIYERHQVQIDHYLGLANKSVKDAMAKIQAKIPGLKRKAD Db 301 ALFNGLTLLILALISLFSIPVIYERHQVQIDHYLGLANKSVKDAMAKIQAKIPGLKRKAD	RESULT 2 US-10-653-20 ; Sequence 20, Application US/10810653 ; Publication No. US20040253218A1 ; Publication No. US20040253218A1 ; APPLICANT: EISENBACH-SCHWARTZ, Michal APPLICANT: BESERANA, Pierre APPLICANT: MOSONEGO, Alon APPLICANT: MOALEM, Gila TITLE OF INVENTION: ACTIVATED T-CELLS, NERVOUS SYSTEM-SPECIFIC ANTIGEN FILE REPERBURES: EIS-SCHWARTZ-ACTIVATED TITLE REPERBURES: EIS-SCHWARTZ-ACTIVATED THEREM APPLICATION NIMPREP. 115/10/810 653	CURRENT FILING DATE: 2004-03-29 PRIOR APPLICATION NUMBER: US/09/893,348 PRIOR FILING DATE: 2001-06-28 PRIOR FILING DATE: 1999-05-19 PRIOR FILING DATE: 1999-05-19 PRIOR FILING DATE: 1998-12-27 PRIOR APPLICATION NUMBER: US 09/218,277 PRIOR APPLICATION NUMBER: PCT/US98/14715 PRIOR APPLICATION NUMBER: PCT/US98/14715	FILING DATE: 1998-05-12 OF SEQ ID NOS: 29 NE: Patentin version 3. NO 20 H: 360 PRT Rattus norvegicus -653-20	Query Match

Ç

118-09-891-348-18	
; Sequence 18, Application US/09893348	7/7
GENERAL INFORMATION (2493AL) ADDITORNE INFORMATION (1707M)	601 LPSAGASVVQPSVSPLEAPPPVSYDSIKLEPENPPPYEEAMNVALKALGTKEGIKEPESF
	Qy 172 171
BESERMAI	Db 661 NAAVQETEAPXISIACDLIKETKLSTEPSPDFSNYSEIAKFEKSVPEHAELVEDSSPESE 720
-CELLS, NERVOUS SYSTEM-SPECIFIC ANTIGENS AND	Qy 172 171
CURRENT FILING DATE: 2001-06-28	Qy 172 171
FRIOR FILING DATE: 1999-05-19 FRIOR APPLICATION NUMBER: 15 09/218 277	Db 781 NLHSTKDAASNDIPTLTKKEKISLQMEEFNTAIYSNDDLLSSKEDKIKESETFSDSSPIE 840
	Oy 172 171
; PRIOR REFLICATION NUMBER: PCJ/US98/14/15 ; PRIOR PILLIO DATE: 1998-07-21 ; DRIOR ADDITRATION NUMBER: TT 13.600	Db 841 IIDEFPTFVSAKDDSPKLAKEYTDLEVSDKSEIANIQSGADSLPCLELPCDLSFKNIYPK 900
FINE FILE DATE: 1998-05-19 FINES OF EF OF TO MOSE. 26	Qy 172 171
; SEO ID NO 18	Db 901 DEVHVSDEFSENRSSVSKASISPSNVSALEPQTEMGSIVKSKSLTKEAEKKLPSDTEKED 960
LENGTH: 1 TYPE: PRT ORGANISM:	Oy 172SVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLS 217
US-09-893-348-18	
Query Match 95.0%; Score 1732.7; DB 9; Length 1163; Best Local Similarity 31.0%; Pred. No. 5.7e-51;. Matches 360: Conservative 0: Mismatches 0: Indels 803: Gans 1:	Qy 218 VTISFRIYKGVIQAIQKEDEGHPRAYLESEVAISEELVQKYSNAALGHVNSTIKELRRL 277
1 MEDIDOSSIVSSSIVSSPREPREPREDEEDEBEBEBEBEBEBEBEBEBEBEBEBEBEBEBEBEB	Gy 278 FLVDDLVDSLKFAVLMWVFTYVGALFNGLTLLILALISLFSIPVIYERHQVQIDHYLGLA 337
Db 1 MEDIDQSSLVSSSTDSPPRPPPAFKYQFVTEPEDEEBEBEBEBEBEBBEBLBVLERK 60	1001
Qy 61 PAAGLSAAAVPPAAAPLLDFSSDSVPPAPRGPLPAAPPARQPSWERSPAAPRSLP 120 bb 61 PAAGLSAAAVPPAAAAPLLDFSSDSVPPAPRGPLPAAPPAAPERQPSWERSPAAPAPSLP 120	Qy 338 NKSVKDAMAKIQAKIPGLKRKAD 360
121 PAAAVLFSKLPEDDEPPARPPPPAGASPLAEPAAPPSTPAAPKRRGSGS	RESULT 5 US-10-810-653-18
121 PAAAVLPSKLPEDDEPPARPPPPAGASPLAEPAAPPSTPAAPKRGSGSVDETLFALP	; Sequence 18, Application US/10810653 ; Publication No. US20040253218Al
Db 181 AASEPVIPSSAEKIMDLMEOPGNTVSSGOEDFPSVLLETAASLPSLSPLSTVSFKEHGYL 240	; GENEKAL INFORMATION: ; APPLICANT: EISENBACH-SCHWARTZ, Michal ; APPLICANT: COHEN. Irun R.
DD 241 GNLSAVSSSEGTIEFTLNEASKELPERATNPFVNRDLAEFSELEYSEMGSSFKGSPKGES 300	; APPLICANT: MOALEM, Gila ; ITILE OF INVENTION: ACTIVATED T-CELLS, NERVOUS SYSTEM-SPECIFIC ANTIGENS AND THEIR US
Qy 172 171	ヹヸ
Db 301 AILVENTKEEVIVRSKDKEDLVCSAALHSPQESPVGKEDRVVSPEKTMDIFNEMQMSVVA 360	; PRIOR APPLICATION NUMBER: US/09/893,348
Qy 172 171	FRION FILING MUMBER 10 09/314,161
Db 361 PVREEYADFKPFEQAWEVKDTYEGSRDVLAARANVESKVDRKCLEDSLEQKSLGKDSEGR 420	FRICK APPLICATION NUMBER: US 09/218,277
Qy 172 171	FALON FALLING DAILS: 1998-12-22 FRIOR PAPLICATION NUMBER: PCT/US98/14715 DETOR PAPER: 1908-07-31
Db 421 NEDASFPSTPEPVKDSSRAYITCASFTSATESTTANTFPLLEDHTSENKTDEKKIEERKA 480	FALON EAPLICATION NUMBER: 11 124500
Qy 172 171	SEQ ID NOS: 29
Db 481 QIITEKTSPKTSNPFLVAVQDSEADYVTTDTLSKVTEAAVSNMPEGLTPDLVQEACESEL 540	; SOLIMAKE: Patentin Verbion 3.1
Qy 172	
Db 541 NEATGTKIAYETKVDLVQTSEAIQESLYPTAQLCPSFEEAEATPSPVLPDIVMEAPLNSL 600	; OKCANISM: Rattus norvegicus US-10-810-653-18

Db 1021 VTISFRIYKGVIQAIQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRL 1080 Qy 278 FLVDDLVDSLKFAVLMMVFTYVGALFNGTLLILALISLFSIPVIYERHQVQIDHYLGLA 337	RESULT 6 US-10-633-423-10 ; Sequence 10, Application US/10633423 ; Publication No. US20040191240A1 ; PublicAL INFORMATION: ; APPLICANT: Tohyama, Masaya	HAPPLICANT: Yamashita, Toshihide TITLE OF INVENTION: COMPOSITION AND METHOD FOR NERVE REGENERATION FILE REFERENCE: 59150-8023.US00 CURRENT APPLICATION NUMBER: US10/633,423 CURRENT FILING DATE: 2003-07-11 PRIOR APPLICATION NUMBER: US 10/427.741	; PRIOR FILING DATE: 2003-04-30 ; PRIOR APPLICATION NUMBER: JP 2003-92923 ; PRIOR FILING DATE: 2003-03-28 ; NUMBER OF SEQ ID NOS: 27 ; SOFTWARE: Patentin version 3.1 ; SEQ ID NO 10	s musculus	Query Match 89.8%; Score 1637; DB 16; Length 1162; Best Local Similarity 29.8%; Pred. No. 1.1e-47; Matches 348; Conservative 2: Mismatches 6; Indels 810; Gaps 4;	MEDIDOSSLVSSSTDSPPRPPAFKYQFVTEPEDEEDEEEEDEEEDEELEKULERK 60	Qy 61 PAAGLSAAAPLLDFSSDSVPPARGPLPAAPBAPBAPBRQFSWERSPAAPBFSLP 120 Db 60 PAAGLSAAPVPP-AAAPLLDFSSDSVPPARRGPLPAAPPTAPBRQFSWERSPAASAFSLP 118	QY 121 PAAAVLPSKLPEDDEPPARPPPARASPLAEPAAPSTPAAPKRRGSGS	177 AASEPVIPSSAEKIMDLKEQPGNTVSSGQEDFPSVLFETAASLPSLSPLSTVSFKEHGYL 23	237 GNLSAVASTEGILEETLNEASKELFEKAINFFVNKESAEFSVLEISEMGSSFNGSFNGES	DD 297 AMLVENTKEEVIVKSKDKEDLVCSAALANPQESPAILTKVVKELGSVMSFEKIMDIFNEMK 356 QY 172	Qy 172
Query Match 95.0%; Score 1732.7; DB 16; Length 1163; Best Local Similarity 31.0%; Pred; No. 5.7e-51; Tindels 803; Gaps 1; Matches 360; Conservative 0; Mismatches 0; Indels 803; Gaps 1; Qy MEDIDOSSIVSSSTDSPRRPPAFKYQFYTEPBEBEBEBEBEBEBEBEBEBELSTRELERK 60 Db Indels 803; Gaps 1; Db Indels 803; Indels 803; Gaps 1; Qy 61 PAAGLSAAAVPPAAAPLLDFSSDSVPPAPRGPLPAAPPAAPAPERQPSWERSPAAPAPSLP 120 Db 61 PAAGLSAAAVVPAAAAPLLDFSSDSVPPAPRGPLPAAPPAAPERQPSWERSPAAPAPSLP 120	Qy 121 PAMAVLPSKLPEDDEPPARPPPPPAGASPLAEPAAPPSTPAAPKRRGSGS	Db 181 AASEPVIPSSAEKIMDLMEQPGNTVSSGQEDFPSVLLETAASLPSLSFLSTVSFKEHGYL 240 Qy 172 171 Db 241 GNLSAVSSSEGTIEETLNEASKELPERATNPFVNRDLAEFSELEYSEMGSSFKGSPKGES 300	301 AILVENTKEEVIVRSKDKEDLVCSAALHSPQESPVGKEDRVVSPEKTMDIFNEMQMSVVA	361 PVREEYADFKPFEGAMEVKDTYEGSRDVLAARANVESKVDRKCLEDSLEQKSLGKDSEGR	Db 421 NEDASFPSTPEPVKDSSRAYITCASFTSATESTTANTFPLLEDHTSENKTDEKKIEERRA 480 Qy 172	481 QIITEKTSPKTSNPFLVAVQDSEADYVTTDTLSKVTEAAVSNMPEGLTPDLVQEACESEL	541 NEATGTKIAYETKVDLVQTSEAIQESLYPTAQLCPSFERAEATPSPVLPDIVMEAPLNSL	601 LPSAGASVVQPSVSPLEAPPPVSYDSIKLEPENPPPYEEAMNVALKALGTKEGIKEPESF 172	QY 172	Db 781 NLHSTKDAASNDIPTLTKKEKISLQMEEFNTAIYSNDDLLSSKEDKIKESETFSDSSPIE 840 Qy 172 171	841 IIDEFPTFVSAKDDSPKLAKEYTDLEVSDKSEIANIQSGADSLPCLELPCDLSFKNIYPK	DD 901 DEVHVSDEFSENRSSVSKASISPSNVSALEPQTEMGSIVKBKSLITKEAEKKLFSDITEKED 960 QY 172SVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLS 217 DD 961 RSLSAVLSABLSKTSVVDLLYWRDIKKTGVFGASLFLLLSLTVFSIVSVTAYIALALLS 1020 QY 218 VTISFRIYKGVIQAIQKSDEGHPFRAYLESEVAISBELVQKYSNSALGHVNSTIKELRRL 277

ξ,

	Qy 172 171	Db 657 EPESFNAAAQEAEAPYISIACDLIKETKLSTEPSPGFSNYSEIAKFEKSVPDHCELVDDS 716	Qy 172 171	DD 717 SPESEPVDLPSDDSIPEVPQTQEEAVMLMKESLTEVSETVTQHKHKERLSASPQEVGKPY 776	Qy 172 171.	Db 777 LESFQPNLHITKDAASNEIPTLTKKETISLQMEEFNTAIYSNDDLLSSKEDKMKESETFS 836	Qy 172 171	DD 837 DSSPIEIIDEFPTFVSAKDDSPKEYTDLEVSNKSEIANVQSGANSLPCSELPCDLSFKNT 896	Qy 172 171	DD 897 YPKDEAHVSDEFSKSRSSVSKVPLLLPNVSALESQIEMGNIVKPKVLTKEAEEKLPSDTE 956	QY 172SVVDLLYWRDIKKTGVV-FGASLFLLLSLTVFSIVSVTAXIAL 213	Oy 214 ALLSVTISFRIYKGVIQALQKSDEGHPFRAYLESFVAISEELVOKYSNSALGHYNSTIKE 273	274 IDDI. PLIMOLIMEL KRAM MANDEMYNCAL BNCLATI. I.A. I.S. PSI DVI VRDHOVOTDHV	1077 LRRLFLVDDLVDSLKFAVLMWVFTYVGALFNGLTLLILALISLFSIPVIYERHQAQIDHY	Qy 334 LGLANKSVKDAMAKIQAKIPGLKRKAD 360		RESULT 9 US-09-789-386-6	; Sequence b, Application US/09/8938b ; Patent No. US2020010324Al	; GENERAL INFORMATION: ; APPLICANT: PRINJHA, RABINDER KUMAR	; TITLE OF INVENTION: NOVEL COMPOUNDS ; FILE REFERENCE: GP-30165-C1		; PRIOR APPLICATION NUMBER: U.K. 9916898.1 ; PRIOR FILING DATE: 1999-07-119	AFFLICATION NOTBER: U.N. 2018023: FILING DATE: 1998-07-22 BDDITCHON NIMBER: HE 09/359 208	PRIOR FILING DATE: 1999-07-22 NUMBER OF SEO ID NOS: 6			; 11E5: FA1 ; ORGANISH HOMO SAPIENS 178-09-789-388-6	-03-703-30-0 -03-703-30-0 -03-04-04-04-04-04-04-04-04-04-04-04-04-04-	s; nemgen	MEDIDOSSIVSSTDSPPRPPAFKXOFVTEPEDEEDEEEBDEEDDEDLEELE	1 MEDLDQSPLVSSS-DSPPRPQPAFKYQFVREPEDEE-EEEEEEEDEDLEELEVLERK	
Db 1077 RRLFLVDDLVDSLKFAVLMMVFTYVGALFNGLTLLJLALISLFSIPVIYERHQAQIDHYL 1136	A TO THE MENTAL MANUE OF THE PARTY OF THE PA	535 CHANNS VLAFARIA GANLE CLINARAD 380 1137 CLIANE CHENTRAL CANTER [1137 GLANNSVADAMANIQANIFGLINKNAE	KESULT 8	US-10-267-502-431 ; Sequence 431, Application US/10267502			; TITLE OF INVENTION: Obesity Linked Genes FILE REFERENCE: LED-07416		NOMBER OF SEQ ID NOS: 439 SOFTWARE PatentIn version 3.2) SM 15 NO 431) LENGTH: 1163 TYPE: PRT) ORGANISM: Mus musculus	89.0%; Score 1622.9; DB	7; Conservative 2	1 MEDIDOSSLVSSTDSPPRPPAFKYQFVTEPEDEEDEBEEEDEEDEELEVLERK	A MEULUQSSLVSSSAUSFFRFFFRFKTÇFVIEFEUEEUEEUEEUEEUEEUEEUEEUEEUEEUEEUEEUEEU	Qy 61 PAAGLSAAAVPLAAAPLLDFSSDSVPPAPRGPLPAAPPRAPERQPSWERSPAAPAPSLP 120	121 PAAAVLPSKI.PEDDEPPARPPPPAGASPI.AEPAAPPSTPAAPKRGSGS	119	AASEPVI PSSAEKIMDLKEQPGNTVSSGQEDFPSVLFETAASLPSLSPLSTVSFKEHGYL	172	Db 237 GNLSAVASTEGTIEETLNEASRELPERATNPFVNRESAEFSVLEYSEMGSSFNGSPKGES 296	Qy 172 171	Db 297 AMLVENTKEEVIVRSKDKEDLVCSAALHNPQESPATLTKVVKEDGVMSPEKTMDIFNEMK 356	Qy 172 171	Db 357 MSVVARVREEYADFKPFEQAWEVKDTYEGSRDVLAARANMESKVDKKCFEDSLEQKSHGK 416	φγ 172 171	Db 417 DSESRNENASFPSTPELVKDGSRAYITCDSFTSATESTAANIFPVLEDHTSENKTDEKKI 476	Ογ 172 171	Db 477 EERKAQIITEKTSPKTSNPFLVAIHDSEADYVTTDNLSKVTEAVVATMPEGLTPDLVQEA 536	Qy 172 171	Db 537 CESELNEATGTKIAYETKVDLVQTSEAIQESIYPTAQLCPSFEEAEATPSPVLPDIVMEA 596	gy 172 171

```
61 PAAGLSAAAVP--PAAAAPLLDFSSDSVPPAPRGPLPAAPPAAPERQPSWERSPAA---P 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              119 APSPLSAAAVSPSKLPEDDEPPARPPPPASVSPQAEPVWTPPAPAAPPSTPAAPKR 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               179 RGSSGSVVVDLLYWRDIKKTGVVFGASLFLLSLITVFSIVSVTAYIALALLSVTISFRIY 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KGVIQAIQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVD 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              299 SLKFAVLMMVFTYVGALFNGLTLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAM 358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SLKFAVLMWVFTYVGALFNGLTLLILALISLFSIPVIYERHQVQIDHYLGLANKSVKDAM 345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 MEDIDQSSLVSSSTDSPPRPPAFKYQFVTEPEDEEDEEBEEBDEBDLBELEVLERK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      116 APSLPPAAAVLPSKLPEDDEPPARPPPPAGASPLAE------PAAPPSTPAAPKR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KGVIQAIQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRLFLVDDLVD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RG-SGSSVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 373;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 87.9%; Score 1603.3; DB 9; Length Best Local Similarity 87.2%; Pred. No. 2.2e-47; Matches 327; Conservative 11; Mismatches 20; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 72, Application US/10060036; Publication No. US20030073144A1; GENERAL INFORMATION: APPLICANT: Benson, Darin R.; APPLICANT: Kalos, Michael D.
    359 AKIQAKIPGLKRKAE 373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AKIQAKIPGLKRKAD 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AKIQAKIPGLKRKAE 373
                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Homo sapiens
                                           RESULT 11
US-09-893-348-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 12
US-10-060-036-72
                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-893-348-24
                                                                                                                                                                                                                                                                                                                                                                                           SEQ ID NO 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  359
  용
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ठ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ď
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          셤
                                166
                                                                                      225
                                                                                                    285
                                                                                                                                                           PAAGLSAAPVPTAPAAGAPLMDFGNDFVPPAPRGPLPAAPPVAPERQPSWDPSPVSSTVP 118
                                                                                                                                                                                                   SLKFAVLMWVFTYVGALFNGLTLLILALISLFSIPVIYERHQVQIDHYLGLANKSVKDAM 345
                                                                                                                                                                                                                  61 PAAGLSAAAVP--PAAAAPLLDFSSDSVPPAPRGPLPAAPPAAPERQPSWERSPAA---P 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SLKFAVLMWVFTYVGALFNGLTLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAM 358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 116 APSLPPAAAVLPSKLPEDDEPPARPPPPPAGASPLAE-----PAAPPSTPAAPKR 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        286 SLKFAVLMWVFTYVGALFNGLTLLILALISLFSIPVIYERHQVQIDHYLGLANKSVKDAM 345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               28
                                           KGVIQAIQKSDEGHPPRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRLFLVDDLVD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KGVIQAIQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRLFLVDDLVD
                                                                                   RG-SGSSVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 MEDIDOSSLVSSSTUSPPRPPPAFKYQFVTEPEDEEDEEDEEDEEDEEDEELEVLERK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RG-SGSSVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Cao, Lit
TITLE OF INVENTION: BONE MARROW SECRETED PROTEINS AND POLYNUCLEOTIDES
FILE REPERENCE: 1458,004/200130,449
CURRENT APPLICATION NUMBER: US/09/765,205
CURRENT FILING DATE: 2001-01-17
PRIOR APPLICATION NUMBER: US/09/212,440
PRIOR FILING DATE: 1998-12-16
NUMBER OF SEQ ID NOS: 46
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 6
LENGTH: 373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 9; Length 373;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .
20;
                            APSLPPAAAVLPSKLPEDDEPPARPPPPAGASPLAE-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 87.9%; Score 1603.3; DB Best Local Similarity 87.2%; Pred. No. 2.2e-47 Matches 327; Conservative 11; Mismatches 2
                                                                                                                                                                                                                                                                                                                                                            Sequence 6, Application US/09765205
Patent No. US20020034800A1
GENERAL INPORMATION:
                                                                                                                                                                                                                                                           346 AKIQAKIPGLKRKAD 360
                                                                                                                                                                                                                                                                            359 AKIQAKIPGLKRKAE 373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                346 AKIQAKIPGLKRKAD 360
|||||||||||||
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: human
US-09-765-205-6
                                                                                                                                                                                                                                                                                                                               RESULT 10
US-09-765-205-6
 29
                                                                                   167
                                                                                                              179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            239
                                                                                                                                            226
                                                                                                                                                                     239
                                                                                                                                                                                                  286
                                                                                                                                                                                                                              299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   299
                                                       유
                                                                                  ò
                                                                                                           임
                                                                                                                                            ઠ
                                                                                                                                                                    g
                                                                                                                                                                                                ઠે
                                                                                                                                                                                                                             ద
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  유
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       요
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   硆
                            ઠે
                                                                                                                                                                                                                                                           ò
                                                                                                                                                                                                                                                                                    셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ઠ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ઠ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ò
```

166

9

Gaps

17;

166

238

```
Sequence 24, Application US/10810653
Sequence 24, Application US/10810653
Sequence 24, Application US/10810653
Publication No. US20040253218A1
GENERAL INFORMATION:
APPLICANT: BISENBACH-SCHWARTZ, Michal
APPLICANT: COHEN, Trun R.
APPLICANT: MOSONEGO, Alon
APPLICANT: MOSONEGO, Alon
APPLICANT: MOSONEGO, Alon
APPLICANT: MOSONEGO, Alon
APPLICANT: MOSONEGO, Alon
APPLICANT: MOSONEGO, Alon
APPLICANT: MOSONEGO, Alon
APPLICANT: MOSONEGO, Alon
APPLICANT: MOSONEGO, Alon
APPLICANT: MOSONEGO, Alon
APPLICANT: MOSONEGO, Alon
APPLICANT: MOSONEGO, Alon
APPLICATION NUMBER: US/09/893,348
PRIOR PILING DATE: 1999-06-19
PRIOR PILING DATE: 1999-06-19
PRIOR PILING DATE: 1999-06-19
PRIOR PILING DATE: 1998-05-19
AUWHERE OF SEQ ID NOS: 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    59 PAAGLSAAPVPTAPAAGAPLMDFGNDFVPPAPRGPLPAAPPVAPERQPSWDFSPVSSTVP 118
                                                                                                                     SLKFAVLMWVFTYVGALFNGLTLLILALISLFSIPVIYERHQVQIDHYLGLANKSVKDAM 345
                                                                                                                                                                                                                                      RG-SGSSVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIY 225
                                                                                                                                                                                                                                                                                                                                                                                               KGVIQAIQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRLFLVDDLVD 285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   299 SLKFAVLMWVFTYVGALFNGLTLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAM 358
                                                    239 KGVIQAIQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                116 APSLPPAAAVLPSKLPEDDEPPARPPPPAGASPLAE------PAAPPSTPAAPKR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 PAAGLSAAAVP--PAAAAPLLDFSSDSVPPAPRGPLPAAPPAAPEROPSWERSPAA---P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 MEDIDQSSLVSSSTDSPPRPPAFKYQFVTEPEDEEDEEEEDEEDDEDLEELEVLERK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 16; Length 373;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             87.9%; Score 1603.3; DB 16; Length
87.2%; Pred. No. 2.2e-47;
ative 11; Mismatches 20; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      346 AKIQAKIPGLKRKAD 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AKIQAKIPGLKRKAE 373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: PatentIn version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 87.2<sup>3</sup>
Matches 327; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-10-810-653-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-10-810-653-24
                                                                                                                                                                                                                                                                                                                                                                                               226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQ ID NO 24
                                                                                                                                                                                                                                                                                                         167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     g
                                                                유
                                                                                                                     δ
                                                                                                                                                           셤
                                                                                                                                                                                                           ઠ
                                                                                                                                                                                                                                               임
                                                                                                                                                                                                                                                                                                       ò
                                                                                                                                                                                                                                                                                                                                                  g
                                                                                                                                                                                                                                                                                                                                                                                               ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                           셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 8, Application US/10408967;
Sequence 8, Application US/10408967;
Publication No. US20040063161A1
GENERAL INFORMATION:
APPLICANT: Pharmacia & Upjohn Company
APPLICANT: Yan, Riqiang
APPLICANT: Lu, Yifeng
TITLE OF INVENTION: Compositions and Methods of Treating Alzheimer's Disease;
FILE REFERENCE: 00925
CURRENT FILING DATE: 2003-04-08
NUMBER OF SEQ ID NOS: 9
SOFTWARE: Patentin version 3.1
SEQ ID NO 8
LENGTH: 373
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9
                                                                                                                                                                                                                                                                                                                                                                                                                                                  9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 PAAGLSAAAVP--PAAAAPLLDFSSDSVPPAPRGPLPAAPPAAPERQPSWERSPAA---P 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SLKFAVLMWVFTYVGALFNGLTLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAM 358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 116 APSLPPAAAVLPSKLPEDDEPPARPPPPAGASPLAE------PAAPPSTPAAPKR 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       119 APSPLSAAVSPSKLPEDDEPPARPPPPASVSPQAEPVWTPPAPAPAAPPSTPAAPKR 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     179 RGSSGSVVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIY 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KGVIQAIQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRLFLVDDLVD 285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         286 SLKFAVLMWVFTYVGALFNGLTLLILALISLFSIPVIYERHQVQIDHYLGLANKSVKDAM 345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RG-SGSSVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 MEDLDQSPLVSSS-DSPPRPQPAFKYQFVREPEDEE-EEEEEEEEDEDEDLEELEVLERK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MEDIDOSSLVSSSTDSPPRPPAFKYQFVTEPEDEEDEEEDEEEDEEDEDLEELEVLERK
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            20; Indels 17; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match

87.9%; Score 1603.3; DB 15; Length 373;
Best Local Similarity 87.2%; Pred. No. 2.2e-47;
Matches 327; Conservative 11; Mismatches 20; Indels 17;
                                                                                                                                                                                                                                                                                                                                                                                                  DB 14; Length 373;
APPLICANT: Lodes, Michael J.
APPLICANT: Persing, David H.
APPLICANT: Hersing, David H.
APPLICANT: Hersing, William T.
APPLICANT: Hersing, Vargiu
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF PANCREATIC CANCER
FILE REPERENCE: 210121.68
CURRENT APPLICATION NUMBER: US/10/060,036
CURRENT FILING DATE: 2002-01-30
NUMBER OF SEQ ID NOS: 4560
SOFTWARE: FastSEQ for Windows Version 4.0
BEQ ID NO 72
LENGTH: 373
                                                                                                                                                                                                                                                                                                                                                                                                                                               20; Indels
                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 87.9%; Score 1603.3; DB Best Local Similarity 87.2%; Pred. No. 2.2e-47; Matches 327; Conservative 11; Mismatches 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               346 AKIQAKIPGLKRKAD 360
                                                                                                                                                                                                                                                                                                       TYPE: PRT
CORGANISM: Homo sapiens
US-10-060-036-72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                , ORGANISM: Homo sapiens
US-10-408-967-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 13
US-10-408-967-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       윰
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  δ
```

115

Search completed: June 23, 2005, 10:34:28 Job time : 113.849 secs

```
--PAAPPSTPAAPKR 166
                                                          225
                                                                                      238
                                                                                                                  KGVIQAIQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRLFLVDDLVD 285
                                                                                                                                  239 KGVIQAIQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVD 298
                                                                                                                                                                            SLKFAVLMWVFTYVGALFNGLTLLILALISLFSIPVIYERHQVQIDHYLGLANKSVKDAM 345
                                                                                                                                                                                           238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SLKFAVLMWVFTYVGALFNGLTLLILALISLFSIPVIYERHQVQIDHYLGLANKSVKDAM 345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               116 APSLPPAAAVLPSKLPEDDEPPARPPPPAGASPLAE------PAAPPSTPAAPKR 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RG-SGSSVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIY 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         28
                                                                                                                                                                                                                                                                                                                                   US-10-34'-080-100

US-10-34'-080-100

US-10-34'-080-100

Equence 6, Application US/10347669

Publication No. US20050084850A1

GENERAL INFORMATION:

APPLICANT: Cao, Li

TITLE OF INVENTION: BONE MARROW SECRETED PROTEINS AND POLYNUCLEOTIDES

FILE REFERENCE: 1458.004/200130.449

CURRENT APPLICATION NUMBER: US/10/347,669

PRIOR APPLICATION NUMBER: US/09/212,440

PRIOR PILING DATE: 1998-12-16

NUMBER OF SEQ ID NOS: 466.4

SOFTWARE: FastSEQ for Windows Version 3.0

SEQ ID NO 6

SEQ ID NO 6

LENGTH: 373

TYPE: RT

ORGANISM: human

US-10-347-669-6
                    RG-SGSSVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIY
                                                                          1 MEDLIDQSPLVSSS-DSPPRPQPAFKYQFVREPEDEE-EEEEEEEDEDEDLEELEVLERK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KGVIQAIQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRLFLVDDLVD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KGVIQAIQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 MEDIDQSSLVSSSTDSPPRPPAFKYQFVTEPEDEEDEEDEEDEEDEEDEELEVLERK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                17; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              87.9%; Score 1603.3; DB 17; Length 373;
87.2%; Pred. No. 2.2e-47;
tive 11; Mismatches 20; Indels 17;
APSLPPAAAVLPSKLPEDDEPPARPPPPAGASPLAE
                                                                                                                                                                                                                                                      346 AKIQAKIPGLKRKAD 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AKIQAKIPGLKRKAD 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 87.24
Matches 327; Conservative
                                                                                                                                                                                                                                                                                                              RESULT 15
US-10-347-669-6
116
                                                                                                                 226
                                                         167
                                                                                                                                                                            286
                                                                                                                                                                                                         299
                                                                                                                                                                                                                                                                 359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    359
                        셤
                                                      8
                                                                             셤
                                                                                                                 ò
                                                                                                                                           요
                                                                                                                                                                          ઠે
                                                                                                                                                                                                    g
                                                                                                                                                                                                                                     ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       요
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            δ
```

This Page Blonk (USDIO)

Human Human

Adu04591 PAD930938 PAD68600 PAD581078 PAD581078 PAD698103 PAD67234 PAD67234 PAT13966 PAD626400 PAD626400 PAD926400 PAD926400 PAD930986

Human neu Human Nog Human Nog Human Nog Human Nog Human RTN Human neu Human neu Human neu Human pen Novel hum Human pol Human pro

Aay71311 Aae03987 Aau33228 Aam93484 Ad131138 Adq16420 Abu11573 Aay95012

Scoring table:

Searched:

Minimum DB Maximum DB

Database

Perfect score:

Sequence:

ı

OM protein

Run on:

Н

```
Rat; neurite growth inhibitor; Nogo A; neural cell; myelin; CNS; central nervous system; neoplastic disease; antiproliferative; glioma; antisense gene therapy; neuroblastoma; menagioma; retinoblastoma; degenerative nerve disease; Alzheimer's disease; Parkinson's disease; hyperproliferative disorder; benign dysproliferative disorder; diagnosis; psoriasis; tissue hypertrophy; neuronal regeneration; treatment; structural plasticity; screening; mutant; mutein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          go proteins and nucleic acids useful for treating neoplastic disorders the central nervous system and inducing regeneration of neurons.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rat Nogo A protein fragment used in the construction of mutant Nogo-B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 .171
/note= "Corresponds to residues 1-171 of rat Nogo
protein shown in AAY71310"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        975-1162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note= "Corresponds to residues protein shown in AAY71310"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ALIGNMENTS
                                                                                                                                                                                                           ADK67502
AAY71311
AAE03987
AAU3328
AAW33484
ADL31138
ADL31138
ADL31138
ADL31138
AQ16420
ABU11573
AAY95012
                                                                                                   ABR59667
ADO08103
ADP45551
                                                                                                                                                                 ADP67234
ADR13966
                                            ABG30938
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAY71558 standard; protein; 359 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example; Page; 122pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    98US-0107446P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          99WO-US026160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  172. .359
11192
11192
11192
11192
11192
11192
11192
11193
11193
11193
11193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Chen MS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2000-400052/34.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (SCHW/) SCHWAB M E. (CHEN/) CHEN M S.
WO200031235-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    06-NOV-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          05-NOV-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               02-NOV-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  02-JUN-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Schwab ME,
                                                                                                                                                                                                                                                                                                                                                           1013.8
1012.1
1010.8
                                                         1518.4
1518.4
1518.4
1518.4
1518.4
1518.4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           g
                                                                                                                                                                                                                                                       1510.8
                                                                                                                                                                                                                                                                                                                       1204.7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAY71558;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rattus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Key
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAY71558
A bone ma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rat neuro
Rat trunc
Rat NogoA
Rat Nogo
Mus muscu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human Nog
Human NOG
Human RTN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human pan
Human neu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human apo
Human RTN
Human Nog
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Rat fooce
Rat neuri
Alternati
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mouse pol
A bone ma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human Nog
Human MAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Alternati
                                                                                                                                                                 (without alignments)
1223.045 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                       1 MEDIDQSSLVSSSTDSPPRP......VKDAMAKIQAKIPGLKRKAD 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Description
                                                                                                                                             June 23, 2005, 10:16:50 ; Search time 113.842 Seconds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Aay71383 E
Abb81076 E
Aay71385 Adb85283 E
Aay71310 E
Aay71310 E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Abb81074
Ado26399
Ady1557
Adx1557
Adx89537
Ado8105
Aay56969
Aay56969
Aab82320
Aab82320
Aam47954
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Abp68601
Abb81079
Adi63044
Adk67503
Adp67235
Abg30937
Aay56967
                                                                                                                                                                                                                                                                                                                                                                                                                             2105692
                 version 5.1.6
- 2005 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                      Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                 2105692 segs, 386760381 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SUMMARIES
                                                                                                     protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAY71558
AAY71383
ABB81076
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAY71310
AAY71384
ABB81074
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AABB2350
AAM47954
ABP68601
ABB81079
ADI63044
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAY71385
ADB85283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AD026399
ADP45572
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADK67503
ADP67235
ABG30937
AAY56967
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADT89537
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AD008105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAY53624
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAY56969
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAB24242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAY71557
                                                                                                                                                                                                                                                                                                                                       Gapop 10.0 , Gapext 0.1
                   GenCore (c) 1993 -
                                                                                                                                                                                                                               US-09-830-972-2-FUSED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                geneseqp2000s:*
geneseqp2001s:*
geneseqp2002s:*
geneseqp2003as:*
geneseqp2003bs:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Geneseg 16Dec04:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Post-processing: Minimum Match 0% Maximum Match 100%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             geneseqp1980s:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               geneseqp1990s:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   seq length: 0
seq length: 200000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      四
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11163
11163
11162
11162
11162
11163
373
373
373
373
373
373
373
373
                                     Copyright
                                                                                                                                                                                                                                                                                                                   BLOSUM62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            \begin{array}{c} \mathbf{4} \\ \mathbf{600} ```

Ø

Nogo

rat

ğ

1817 1812.9 1808.1 1732.7 1732.7 1732.7 1732.7 1732.7 1637.7 1622.9

Score

Result Š. 1603.3 1603.3 1603.3 1603.3 1603.3 1603.3

1603.3 1603.3 1595.3 1518.4

retinoblastoma;

```
Thiribitory activity are used in the treatment of neoplastic disease of the CNS e.g. glioma, glioblastoma, medulloblastoma, craniopharyngioma, ependyoma, pinealoma, haemangioblastoma, acoustic neuroma, coligodendroglioma, menagioma, neuroblastoma or retinoblastoma and degenerative nerve diseases e.g. Alzheimer's and Parkinson's diseases. Therapeutics which promote Nogo activity can be used to treat or prevent hyperproliferative or benign dysproliferative disorders e.g. psoriasis and tissue hypertrophy. Ribozymes or antisense Nogo nucleic acids can be used to inhibit production of Nogo protein to induce regeneration of neurons or to promote structural plasticity of the CNS in disorders where neurons or to promote structural plasticity of the CNS in disorders where neurons or to promote structural plasticity of the CNS in disorders where neurons or to promote structural plasticity of the CNS in disorders where neurons or to promote structural plasticity of the CNS in disorders where animal models can be used in diagnostic and screening methods for treat or prevent disorders and to screen for or test molecules which can treat or prevent disorders or diseases of the CNS. The present sequence is derived by fusing two fragments of rat Nogo A protein shown in AAY1310. The fragment is used in the construction of mutant Nogo-B. The mutant is composed of His-tagy/rector/Nogo-A sequence as al-171 + 975-1162. Nogo protein. Major inhibitory region was identified in the Nogo and History and protein shown in AAY1310. The distinction but is derived from rat Nogo A sequence is not given in the Second S
 patent relates to neurite growth inhibitor Nogo which is free of all
 central nervous system (CNS) myelin material with which it is natively associated. Nogo proteins and fragments displaying neurite growth inhibitory activity are used in the treatment of neoplastic disease of
8888888888888888888888888888888888888
```

Sequence 359 AA;

```
120
 180
 180
 240
 240
 PAAGLSAAAVPPAAAAPLLDFSSDSVPPAPRGPLPAAPPAAPERQPSWERSPAAPAFSLP 120
 FRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRLFLVDDLVDSLKFAVLMWVFTYVG 300
 9
 9
 301 ALFNGLTLILLALISLFSIPVIYERHQVQIDHYLGLANKSVKDAMAKIQAKIPGLKRKA 359
 ALFNGLTLLILALISLFSIPVIYERHQVQIDHYLGLANKSVKDAMAKIQAKIPGLKRKA 359
 1 MEDIDQSSLVSSSTDSPPRPPPAFKYQFVTEPEDEEEEEEEEEEDEEEEEDEELEELEVLERK
 PAAGLSAAAVPPAAAAPLLDFSSDSVPPAPRGPLPAAPPAAPERQPSWERSPAAPAPSLP
 PAAAVLPSKLPEDDEPPARPPPPAGASPLAEPAAPPSTPAAPKRRGSGSSVVDLLYWR
 121 PAAAVLPSKIPEDDEPPARPPPPAGASPLAEPAAPPSTPAAPKRRGSGSSVVDLLYWR
 DIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQAIQKSDEGHP
 1 MEDIDQSSLVSSSTDSPPRPPAFKYQFVTEPEDEEDEEEEBDEEDDEDLEELEVLERK
 DIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQAIQKSDEGHP
 Gaps
 ;
0
99.7%; Score 1817; DB 3; Length 359; 100.0%; Pred. No. 3e-65;
 0; Indels
 100.0%; Pred. ...
 Matches 359; Conservative
 Local Similarity
 61
 121
 61
 181
 301
Query Match
 181
 241
 QQ
 g
 g
 à
 셤
 ò
 ઠે
 ò
 g
 ò
 ద
```

```
Rat; neurite growth inhibitor; Nogo B; neural cell; myelin; CNS; central nervous system; neoplastic disease; antiproliferative; glioma;
 Rat neurite growth inhibitor Nogo B.
 AAY71383 standard; protein; 360 AA
 02-NOV-2000 (first entry)
AAY71383
ID AAY7
XX
AC AAY7
XX
DT 02-N
XX
DE RAT
XX
XX
XX
XX
```

degenerative nerve disease; Alzheimer's disease; Parkinson's disease; ypperproliferative disorder; benign dysproliferative disorder; diagnosis; psoriasis; tissue hypertrophy; neuronal regeneration; treatment; structural plasticity; screening. The present sequence is a rat Nogo B protein which is a potent neural cell growth inhibitor and is free of all central nervous system (CNS) meyelin material with which it is natively associated. The Nogo B transcript arises as a result of alternative splicing of Nogo gene. Nogo proteins and fragments displaying neurite growth inhibitory activity are used in the treatment of neoplastic disease of the CNS e.g. glioma, glioblastoma, medulloblastoma, craniopharyngioma, ependyoma, pinealoma, haemangioblastoma, acoustic neuroma, oligodendroglioma, menagioma, neuroblastoma and degenerative nerve diseases e.g. Alzheimer's and Parkinson's diseases. Therapeutics which promote Nogo activity can be used to treat or prevent hyperproliferative or benign dysproliferative disorders e.g. psoriasis and tissue hypertrophy. Nogo proteins and nucleic acids useful for treating neoplastic disorders of the central nervous system and inducing regeneration of neurons. /note= "Corresponds to C-terminal 188 amino acids (residues 976-1163) of Nogo A protein (AAY71310). This region is common to Nogo A, B and C isoforms" 185. .220
11ab-1 - Transmembrane domain /note= "C-terminal hydrophobic region" amino acids 1-172 of Nogo note= "Inhibits NIH 3T3 fibroblast spreading" note= "Protein kinase C (PKC) site" 287. .322
/label= Transmembrane domain
/note= "C-terminal hydrophobic note= "Casein kinase II site" 'note= "Protein kinase C (PKC) 'note= "Protein kinase C (PKC) /note= "Protein kinase C (PKC) 268. .270 /note= "Asn is N-glycosylated" 'note= "Asn is N-glycosylated" protein shown in AAY71310" "Corresponds to "Acidic region" Location/Qualifiers Example; Page; 122pp; English. 98US-0107446P. 173. .360 31. .58 /note= "1 1. .172 /note= " WPI; 2000-400052/34. (SCHW/) SCHWAB M E. (CHEN/) CHEN M S. Inhibitory-site WO200031235-A2 Modified-site Modified-site Modified-site Modified-site Modified-site Modified-site Modified-site 05-NOV-1999; 06-NOV-1998; 02-JUN-2000. Schwab ME, Rattus sp Region Region Domain Domain Region 

```
Discourage of an execution of neutrons or to production of Nogo protein to induce regeneration of neutrons or to promote structural plasticity of the CNS in disorders where neurite growth, regeneration or maintenance are deficient or desired. The animal models can be used in diagnostic and screening methods for predisposition to disorders and to screen for or test molecules which can treat or prevent disorders or diseases of the CNS. Note: The present sequence is not given in the specification but is derived from Nogo A protein sequence (AAY71310) and corresponds to residues 1-172 fused to 976-1163 of Nogo A. The specification claims an alternative version of this sequence (see AAY71385.) which corresponds to residues 1-172 fused to 976-1163 of Nogo A. SEQ ID numbers 35-42 are referred in claim 32 and SEQ ID No. 29 in disclosure of the specification. However the specification does not include sequences for these SEQ ID numbers
 Ribozymes or antisense Nogo nucleic acids can be used to inhibit
8888888888888888888888888
```

Sequence 360 AA;

```
120
 120
 180
 180
 240
 240
 FRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRLFLVDDLVDSLKFAVLMWVFTYVG 300
 300
 ALFNGLTLLILALISLFSIPVIYERHQVQIDHYLGLANKSVKDAMAKIQAKIPGLKRKAD 360
 360
 9
 9
 61 PAAGLSAAAVPPAAAAPLLDFSSDSVPPAPRGPLPAAPPRAPERQPSWERSPAAPASLP
 121 PAAAVLPSKIPEDDEPPARPPPPAGASPLAEPAAPPSTPAAPKRRGSGSVVVDLLYWR
 FRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRLFLVDDLVDSLKFAVLMWVFTYVG
 ALFNGLTLLILALISLFSIPVIYERHQVQIDHYLGLANKSVKDAWAKIQAKIPGLKRKAD
 MEDIDQSSLVSSSTDSPPRPPPAFKYQFVTEPEDEEDEEEEDEEEDDEDLEELEVLERK
 PAAGLSAAAVPPAAAAPLLDFSSDSVPPAPRGPLPAAPPAAPEROPSWERSPAAPAPSLP
 PAAAVLPSKLPEDDEPPARPPPPAGASPLAEPAAPPSTPAAPKRRGSGSSVVDLLYWR
 DIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQAIQKSDEGHP
 MEDIDQSSLVSSSTDSPPRPPPAFKYQFVTEPEDEEDEEEEEDDEEDLEELEVLERK
 0; Gaps
Score 1817; DB 3; Length 360;
Pred. No. 3e-65;
0; Mismatches 1; Indels
 99.78;
 Matches 359; Conservative
 Query Match
Best Local Similarity
 121
 241
 241
 301
 301
 181
 181
 셤
 ద
 셤
 g
 셤
 g
 ઠ
 ò
 ò
 ò
 8
 Š
```

ABB81076 standard; protein; 360 RESULT 3 ABB81076 

Ş

05-NOV-2002 (first entry)

neurotransmitter receptor protein Nogo-B.

Nerve regeneration, neuroprotection, neuronal degeneration; CNS; PNS; central nervous system; peripheral nervous system; tranquillizer; Nogo; vulnerary; cerebroprotective; anti-tumour; antidiabetic; anticonvulsant; nootropic; antiparkinsonian; ophthalmological; analgesic; hepatotropic; osteopathic; vasotropic; nephrotropic; cytostatic; antigen; gene therapy; neurotransmitter receptor; rat; receptor

Rattus norvegicus

US2002072493-A1

13-JUN-2002

28-JUN-2001; 2001US-00893348

98IL-00124500 98WO-US014715 19-MAY-1998; 21-JUL-1998;

```
The invention relates to promoting nerve regeneration or conferring neuroprotection and preventing or inhibiting neuronal degeneration in the central/peripheral nervous system (NS). The method involves administering NS-specific antigen, its analogue or its peptide, a nucleotide sequence the NS-specific antigen or its analogue or combinations. The method is useful for promoting nerve regeneration and preventing neuronal degeneration in central/peripheral nervous system from injury/disease, where the injury is spinal cord injury, blunt crown injury/disease, where the injury is spinal cord injury, blunt crown injury/disease, where the injury is spinal cord injury, blunt crown injury/disease, where the injury is spinal cord injury, blunt crown injury/disease, where the injury is spinal cord injury, blunt crown injury/disease, where the injury is spinal cord injury, blunt crown injury/disease or neoplasm. The disease results in a degenerative crown injury/disease or neoplasm. The disease results in a degenerative crown aucoimmund disease or neoplasm. The disease is not an aucoimmund disease or neoplasm. The disease is not a disease, facial nerve (Bell's) play, glaucoma, Huntington's chorea, amyotrophic lateral sclerosis, non-arteritic optic neuropathy, and vitamin deficiency, intervertebral dise heritation, prion diseases such as Creutzfeldt-Jakob disease, carpal tunnel syndrome, peripheral crowpathies associated with various diseases, including but not limited contropathy, chronic ataxic neuropathy, billary cirrhosis, primary amyloidosis, obstructive lung diseases, acromegaly, malabsorption crompathies, complications of various drugs acromegaly, malabsorption crompathies, complications of various drugs (e.g., metronidazole) and toxins (e.g., alcohol or organophosphates), Charcot-Marie-Tooth disease, readrenomyeloneuropathy, Giant axonal neuropathy, Refeuw's disease, or lipoproteinemia. The processing contropathy and acaria metaperses represent sequence represents the ratery contropathy.
 Cohen IR, Beserman P, Mosonego A;
 nerve regeneration and preventing neuronal degeneration in
 central/peripheral nervous system from injury/disease, comprises administering nervous system-specific activated T cells/antigen, or
 Example 5; Page 47-48; 93pp; English.
 Hauben E,
98US-00218277.
99US-00314161.
 CO LTD
 (YEDA) YEDA RES & DEV
 Eisenbach-Schwartz M,
 WPI; 2002-607255/65
 N-PSDB; ABN86600.
 analogs/peptides
22-DEC-1998;
19-MAY-1999;
 Moalem G;
```

the

Sequence 360 AA;

8 엄 ઠ g Š g ð 셤 ò 셤

antigen

ö 240 240 241 FRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRLFLVDDLVDSLKFAVLMMVFTYVG 300 241 FRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRLFLVDDLVDSLKFAVLMMVFTYVG 300 PAAGLSAAAVPPAAAAPLLDFSSDSVPPAPRGPLPAAPPAAPERQPSWERSPAAPAPSLP 120 PAAAVLPSKLPEDDEPPARPPPPAGASPLAEPAAPPSTPAAPKRGSGSSVVDLLYWR 180 121 PAAAVLPSKLPEDDEPPARPPPPPAGASPLAEPAAPPSTPAAPKRKGSGSVVVDLLYWR 180 09 9 1 MEDIDQSSLVSSSTDSPPRPPAFKYQFVTEPEDBEBEBEBEBEBDBBLBBLBVLERK · 1 MEDIDOSSLVSSSTDSPPRPPPAFKYQFVTBPEDEEDEEDEEDEEDEEDDEDLEELEVLERK PAAGLSAAAVPPAAAAPLLDFSSDSVPPAPRGPLPAAPPAAPERQPSWERSPAAPAFSLP DIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQAIQKSDEGHP DIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQAIQKSDEGHP Gaps ö 99.7%; Score 1817; DB 5; Length 360; 99.7%; Pred. No. 3e-65; ive 0; Mismatches 1; Indels Matches 359; Conservative Local Similarity 61 61 121 181 181 Query Match Best Local &

```
RESULT 5
ADB85283
임
 엄
 g
 δ
 d
 g
 8
 ð
 δ
 ò
 ð
 ò
 ALFNGLTLLILALISLFSIPVIYERHQVQIDHYLGLANKSVKDAMAKIQAKIPGLKRKAD 360
 Rat; neurite growth inhibitor; Nogo B; neural cell; myelin; CNS; central nervous system; neoplastic disease; antiproliferative; glioma; antisense gene therapy; neuroblastoma; menagioma; retinoblastoma; degenerative nerve disease; Alzheimer's disease; Parkinson's disease; hyperproliferative disorder; benign dysproliferative disorder; penign dysproliferative disorder; penign dysproliferative disorder; penignosis; psoriasis; tissue hypertrophy; neuronal regeneration; treatment;
 /note= "Corresponds to amino acids 975-1163 of Nogo A protein (AAY71310)"
 /note= "Corresponds to amino acids 1-172 of Nogo protein shown in AAY71310"
 .74. .361
note= "This region is common to Nogo A, B and
 note= "Inhibits NIH 3T3 fibroblast spreading"
 Alternative version of rat neurite growth inhibitor Nogo B.
 note= "C-terminal hydrophobic region"
 region
 site"
 1988. 1323
Tlabel= Transmembrane domain
note= "C-terminal hydrophobic
139. 341
 note= "Protein kinase C (PKC)
 'note= "Protein kinase C (PKC)
 note= "Protein kinase C (PKC)
 note= "Protein kinase C (PKC)
 'note= "Asn is N-glycosylated"
 'note= "Casein kinase II site"
 'note= "Asn is N-glycosylated'
 Transmembrane domain
 31. .58
/note= "Acidic region"
173. .361
 Location/Qualifiers
1. .172
 AAY71385 standard; protein; 361 AA
 structural plasticity; screening
 98US-0107446P
 02-NOV-2000 (first entry)
 soforms"
 186. .221
/label= T:
 .271
 Chen MS;
 (SCHW/) SCHWAB M (CHEN/) CHEN M S.
 Inhibitory-site
 WO200031235-A2
 Modified-site
 Modified-site
 Modified-site
 Modified-site
 Modified-site
 Modified-site
 Modified-site
 06-NOV-1998;
 02-JUN-2000
 Schwab ME,
 вb
 301
 AAY71385;
 Rattus
 Region
 Region
 Region
 Domain
 Domain
 Region
 AAY 1385

IID AAY 7

XXX AAY 7

XXX AAY 7

XXX AAY 7

XXX Rat,

XX
 RESULT
 셤
 ð
```

```
The present sequence is an alternative version of rat Nogo B protein
which is a potent neural cell growth inhibitor and is free of all central
cc which is a potent neural cell growth inhibitor and is free of all central
cc nervous system (CNS) myelin material with which it is natively
cassociated. The Nogo B transcript arises as a result of alternative
cg growth inhibitory activity are used in the treatment of neoplastic
cd isease of the CNS e.g. glioma, glioblastoma, medulloblastoma, acoustic
clienzoma, oligodendroglioma, menagioma, neuroblastoma, acoustic
cneuroma, oligodendroglioma, menagioma, neuroblastoma, acoustic
corporative nerve diseases e.g. Alzheimer's and Parkinson's
corporative nerve theory activity can be used to treat
cc disease. Therapeutics which promote Nogo activity can be used to treat
cc or prevent hyperproliferative or benign dysproliferative disorders e.g.
cp coriasis and tissue hypertrophy. Nibozymes or antisense Nogo nucleic
cacids can be used to inhibit production of Nogo protein to induce
cc acids can be used to inhibit production of structural plasticity of the CNS in
cacids where neurite growth, regeneration or maintenance are deficient
cor desired. The animal models can be used in diagnostic and screening
cc desired from Nogo A protein sequence (SARY1310) and corresponds to
cresidues 1-172 fused to 975-1163 of Nogo A. This sequence is an
cereidues 1-172 fused to 975-1163 of Nogo A. This sequence is an
cereidues 1-172 fused to 975-1163 of Nogo A. SEQ ID numbers 35-42 are referred in
cacids (residues 976-1163) of Nogo A. SEQ ID numbers SEQ ID numbers
cc the specification does not include sequences for these SEQ ID numbers
 179
 300
 240
 9
 Nogo proteins and nucleic acids useful for treating neoplastic disorders of the central nervous system and inducing regeneration of neurons.
 241 PFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRLFLVDDLVDSLKFAVLMWVFTYV
 1 MEDIDQSSLVSSSTDSPPRPPAFKYQFVTEPEDEBEBEBEBEBEBDBDLBELEVLERK
 61 PAAGLSAAAVPPAAAAPLLDFSSDSVPPAPRGPLPAAPPAAPERQPSWERSPAAPAPSLP
 PAAAVLPSKLPEDDEPPARPPPPAGASPLAEPAAPPSTPAAPKRRGSGS-SVVDLLYW
 1 MEDIDQSSLVSSSTDSPPRPPAFKYQFVTEPEDEEDEEDEEBEBDBEDLEELEVLERK
 PAAGLSAAAVPPAAAAPLLDFSSDSVPPAPRGPLPAAPPAAPFRQPSWERSPAAPASLP
 RDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQAIQKSDEGH
 PFRAYLESEVAISEELVOKYSNSALGHVNSTIKELRRLFLVDDLVDSLKFAVLMWVFTYV
 GALFNGLTLLILALISLFSIPVIYERHQVQIDHYLGLANKSVKDAMAKIQAKIPGLKRKA
 Gaps
 ;
;
 99.4%; Score 1812.9; DB 3; Length 361; 99.7%; Pred. No. 4.4e-65; rive 0; Mismatches 0; Indels 1;
 Claim 4; Page; 122pp; English.
 Matches 360; Conservative
 Query Match
Best Local Similarity
WPI; 2000-400052/34.
 Sequence 361 AA;
 D 360
 361
 -0
 240
 61
 121
 180
 360
 300
 361
```

```
(first entry)
 31. .57
/note= "F
 activity"
 .58
 note=
 Inhibitory-site
 Misc-difference
 Inhibitory-site
Modified-site
 Modified-site
 Modified-site
 Modified-site
 Modified-site
 Modified-site
 Modified-site
 Modified-site
 Modified-site
 Modified-site
 Modified-site
 02-NOV-2000
 Rattus sp
 342
 361
 AAY71310;
 282
 Peptide
 Region
 Region
 Region
 AAY71310
 유
 ò
 셤
 ò
 g
 ઠે
 Use of gene sequence that is down-regulated in response to streptozocin-
induced diabetes, vector, host cell, animal, polypeptide and antibody, in
screening of compounds for treating or diagnosing pain.
 regulated in the spinal cord in response to streptozocin-induced diabetes, or comprising, hybridising or having at least 80% sequence bhose the sequence whose expression products are kinases, phosphatases, ion channel proteins, receptors, transporters, G-protein coupled receptor proteins, DNA-binding proteins, proteases or enzymes, given in the specification. A gene of the invention has analgesic activity, and may have a use in gene therapy. The gene sequences, vector, host cell, animal, polypeptide and antibody are useful for screening of compounds for diagnosing or treating pain. The kits are useful for simultaneous, separate or sequenced in the spinal cord of a mammal in response to streptozocin-induced diabetes. The compound or pharmaceutical
 PAAGLSAAAVPPAAAAPLLDFSSDSVPPAPRGPLPAAPPAAPERQPSWERSPAAPAFLP 120
 120
 PAAAVLPSKLPEDDEPPARPPPPPAGASPLAEPAAPPSTPAAPKRRGSG------ 170
 121 PAAAVLPSKLPEDDEPPARPPPPPAGASPLAEPAAPPSTPAAPRARGSGSVDETLFALP 180
 -----SSVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTIS 221
 9
 9
 composition is useful as a medicament for treating or diagnosing pain.
The present sequence represents a protein encoded by a gene of the
 MEDIDQSSLVSSSTDSPPRPPPAFKYQFVTBPEDEEEBEBEEEDEEEDDEDLEELEVLERK
 PAAGLSAAAVPPAAAAPLLDFSSDSVPPAPRGPLPAAPPAAPERQPSWERSPAAPALD
 1 MEDIDOSSLVSSSTDSPPRPPARKYQFVTEPEDEEDEEEEEDDEDLEELEVLERK
 invention relates to a novel isolated gene sequence that is down-
 rat; streptozocin; kinase; phosphatase; ion channel protein; recepto:
transporter; G-protein coupled receptor; GPCR; DNA-binding proteins;
 DB 7; Length 379;
 protease; enzyme; analgesic; gene therapy; pain; diabetes
 Indels
 Score 1808.1; DB 7;
Pred. No. 7.5e-65;
1; Mismatches 0;
 Pinnock RD
 Disclosure; Page 239-240; 256pp; English.
 Rat foocen-m2 reticulon SEQ ID NO:164.
 Ş
 χ,
 standard; protein; 379
 Lee
 26-JUL-2002; 2002EP-00255228.
 27-JUL-2001; 2001GB-00018354.
 99.2%;
94.7%;
 (first entry)
 (WARN) WARNER LAMBERT CO.
 Dixon AK,
 Best Local Similarity 94.7
Matches 359; Conservative
 WPI; 2003-364994/35.
N-PSDB; ADB85284.
 Rattus norvegicus
 Sequence 379 AA;
 Brooksbank RA,
 EP1284297-A2
 04-DEC-2003
 19-FEB-2003.
 ADB85283;
 61
 ADB85283
 61
 121
 171
 Query Match
셤
 Š
 g
 g
 8
 ઠ
 ઠે
```

```
241 FRIYKGVIQAIQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRLFLVD 300
 DLVDSLKFAVLMWVFTYVGALFNGLTLLILALISLFSIPVIYERHQVQIDHYLGLANKSV 341
 Rat; neurite growth inhibitor; Nogo A; neural cell; myelin; CNS; central nervous system; neoplastic disease; antiproliferative; glioma; antisense gene therapy; neuroblastoma; menagioma; retinoblastoma; degenerative nerve disease; Alzheimer; disease; Parkinson's disease; hyperproliferative disorder; benign dysproliferative disorder; ponign dysproliferative disorder; piagnosis; psoriasis; tissue hypertrophy; neuronal regeneration; treatment;
181 AASEPVIPSSAVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTIS 240
 281
 623. .640
/note= "used as immunogen to generate antibody AS 472"
626
 FRIYKGVIQAIQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRLFLVD
 172. .259 This region is not essential for inhibitory
 "Region specifically described in claim 16"
 'note= "Inhibits NIH 3T3 fibroblast spreading"
 gite"
 site"
 note= "Protein kinase C (PKC)
 note= "Protein kinase C (PKC)
 note= "Protein kinase C (PKC)
 242. .244
/note= "Asn is N-glycosylated"
 note= "Protein kinase C (PKC)
 'note= "Casein kinase II site"
 (PKC)
 note= "Asn is N-glycosylated"
 note= "Protein kinase C
 'note= "Protein kinase C
 note= "Casein kinase II
 note= "Encoded by TTG"
 "Acidic region"
 Rat neurite growth inhibitor Nogo A.
 Location/Qualifiers
1. .171
 AAY71310 standard; protein; 1163 AA
 KDAMAKIQAKIPGLKRKAD 360
 structural plasticity; screening
 KDAMAKIQAKIPGLKRKAD 379
```

ဖ

```
The present sequence is a rat Nogo A protein which is a potent neural cell growth inhibitor and is free of all central nervous system (CNS) myelin material with which it is natively associated. The protein was derived from a cDNA generated by fusing ROBU37-3, R1-3U21 cDNAs isolated from hexanucleotides-primed rat brain stem/spinal cord library, and Oli18 con A consideration of the control of t
 production of Nego protein to induce regeneration of neurons or to production of Nego protein to induce regeneration of neurons or to promote structural plasticity of the CNS in disorders where neurite growth, regeneration or maintenance are deficient or desired. The animal models can be used in disgnostic and screening methods for predisposition to disorders and to screen for or test molecules which can treat or prevent disorders or diseases of the CNS. Note: The present sequence designated as SEQ ID NO: 2 is stated to be the same as the sequence shown in Fig. 13 (see AAY71384) of the specification. However, this sequence referred in claim 32 and SEQ ID NO: 29 in disclosure of the sequence specification. However, the specification does not include sequences for
 481 QIITEKTSPKTSNPFLVAVQDSEADYVTTDTLSKVTEAAVSNMPEGLTPDLVQEACESEL 540
 PAAGLSAAAVPPAAAAPLLDFSSDSVPPAPRGPLPAAPPAAPERQPSWERSPAAPASLP 120
 301 AILVENTKEEVIVRSKDKEDLVCSAALHSPQESPVGKEDRVVSPEKTMDIFNEMQMSVVA 360
 241 GNLSAVSSSEGTIEETLNEASKELPERATNPFVNRDLAEFSELEYSEMGSSFKGSPKGES 300
 1 MEDIDQSSLVSSSTDSPPRPPPPAFKYQFVTEPEDEEDEEEEEDEEEEDBEEDDEDLEELEVLERK
 PAAGLSAAAVPPAAAAPLLDFSSDSVPPAPRGPLPAAPPAAPERQPSWERSPAAPAPSLP
 PAAAVLPSKLPEDDEPPARPPPPPAGASPLAEPAAPPSTPAAPKRRGSGS------
 181 AASEPVIPSSAEKIMDLMEQPGNTVSSGQEDFPSVLLETAASLPSLSPLSTVSFKEHGYL
 1 MEDIDOSSLVSSSTDSPPRPPARKYQFVTEPEDEEDEEEEEBDEEDDEDLEELEVLERK
 361 PVREEYADFKPFEQAWEVKDTYEGSRDVLAARANVESKVDRKCIEDSLEQKSLGKDSEGR
 421 NEDASFPSTPEPVKDSSRAYITCASFTSATESTTANTFPLLEDHTSENKTDEKKIEERKA
 the central nervous system and inducing regeneration of neurons.
 Score 1732.7; DB 3; Length 1163;
Pred. No. 5.7e-61;
0; Mismatches 0; Indels 803;
 Claim 3; Fig 2A; 122pp; English.
 95.0%;
31.0%;
 Query Match
Best Local Similarity 31.0
Matches 360; Conservative
 these SEQ ID numbers
 Sequence 1163 AA;
 61
 121
 61
 172
 172
 요
 g
 셤
 g
 à
 g
 g
 ð
 셤
 ò
 à
 ò
 ઠે
 ò
 ð
 ઠે
 76. .1163 note= "C-terminal common region found in Nogo A, B and C
 Nogo proteins and nucleic acids useful for treating neoplastic disorders
 note= "used as immunogen to generate antibody AS Bruna"
 note= "This region is not essential for inhibitory
 988. .1023
/label= Transmembrane_domain
/note= "C-terminal hydrophobic region specifically
described in claim 16"
 /label= Transmembrane domain
/note= "C-terminal hydrophobic region specifically
described in claim 16"
 note= "PKC and casein kinase. II sites"
 note= "PKC and casein kinase II sites"
'note= "Protein kinase C (PKC) site"
 note= "Protein kinase C (PKC) site"
 note= "Protein kinase C (PKC) site"
 site"
 site"
 note= "Protein kinase C (PKC)
 note= "Protein kinase C (PKC)
 'note= "Protein kinase C (PKC)
 note= "Protein kinase C (PKC)
 note= "Protein kinase C (PKC)
 note= "Protein kinase C (PKC)
 note= "Casein kinase II site"
 note= "Asn is N-glycosylated"
 note= "Protein kinase C (PKC)
 note= "Asn is N-glycosylated"
 'note= "Casein kinase II site"
 note= "Protein kinase C (PKC)
 note= "Asn is N-glycosylated"
 071. .1073
note= "Asn is N-glycosylated"
 note= "Asn is N-glycosylated"
 99WO-US026160
 98US-0107446P
 75. .1162
 .696
 .914
 .927
 soforms
 ctivity
 Chen MS
 WPI; 2000-400052/34.
 (SCHW/) SCHWAB M E. (CHEN/) CHEN M S.
 N-PSDB; AAD01173
 WO200031235-A2
 Modified-site
 Modified-site
 Modified-site
 Modified-site
 Modified-site
 Adified-site
 Modified-site
 Modified-site
 Modified-site
 Modified-site
 Modified-site
 Modified-site
 Modified-site
 Modified-site
 Modified-site
 Modified-site
 Modified-site
 Modified-site
 Modified-site
 05-NOV-1999;
 06-NOV-1998;
 02-JUN-2000
 Schwab ME,
 Peptide
 Domain
 Region
 Domain
 Region
```

ä

9 9 420

171

```
note= "used as immunogen to generate antibody AS Bruna"
 /label= Unknown
/note= "There is Lys at this position in the sequence
shown in AAY71310"
 note= "There is Ile at this position in the sequence shown in AAY71310"
 note= "There is Asn at this position in the sequence shown in AAY71310"
 Leu at this position in the sequence
 note= "There is Leu at this position in the sequence
172. .259
/note= "This region is not essential for inhibitory
 'note= "used as immunogen to generate antibody
 /note= "PKC and casein kinase II sites"
956
/note= "PKC and casein kinase II sites"
 note= "Protein kinase C (PKC) site"
 site"
 note= "Protein kinase C (PKC) site"
 site"
 note= "Protein kinase C (PKC) site"
 site"
 note= "Protein kinase C (PKC) site"
 note= "Protein kinase C (PKC) site'
 note= "Protein kinase C (PKC)
 note= "Protein kinase C (PKC)
 note= "Protein kinase C (PKC)
 (PKC)
 "Protein kinase C (PKC)
 note= "Protein kinase C (PKC)
 468. .470
/note= "Asn is N-glycosylated"
 "Casein kinase II site"
 94. .696
note= "Asn is N-glycosylated"
 note= "Protein kinase C (PKC)
 note= "Casein kinase II site"
 (PKC)
 "Asn is N-glycosylated"
 note= "Asn is N-glycosylated"
 note= "Casein kinase II site"
 note= "Asn is N-glycosylated"
 note= "Protein kinase C
 = "Casein kinase II .722
 note= "Protein kinase C
 /note= "There is L
shown in AAY71310"
 shown in AAY71310"
 label= Unknown
 activity"
 . 244
 note=
 note=
 note=
 note=
 Inhibitory-site
Modified-site
 Misc-difference
 Misc-difference
 Misc-difference
 Misc-difference
 Misc-difference
 Modified-site
 Modified-site
 Modified-site
 Modified-site
 Modified-site
 Modified-site
 Modified-site
 Modified-site
 Modified-site
 Modified-site
 Modified-site
 Modified-site
 Modified-site
 Modified-site
 Modified-site
 Modified-site
 Modified-site
 Modified-site
 Modified-site
 Modified-site
 Modified-site
 Modified-site
 Modified-site
 Peptide
 Peptide
 Region
 RSLSAVLSAELSKTSVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLS 1020
 FLVDDLVDSLKFAVLMWVFTYVGALFNGLTLILIALISLFSIPVIYERHQVQIDHYLGLA 1140
 960
 277
 171
 900
 171
 171
 661 NAAVQETEAPYISIACDLIKETKLSTEPSPDFSNYSEIAKFEKSVPEHAELVEDSSPESE 720
 171
 780
 171
 781 NLHSTKDAASNDIPTLTKKEKISLOMEEFNTAIYSNDDLLSSKEDKIKESETFSDSSPIE 840
 171
 171
 217
 FLVDDLVDSLKFAVLMWVFTYVGALFNGLTLLILALISLFSIPVIYERHQVQIDHYLGLA 337
 Rat; neurite growth inhibitor; Nogo A; neural cell; myelin; CNS; central nervous system; neoplastic disease; antiproliferative; glioma; antisense gene therapy; neuroblastoma; menagioma; retinoblastoma; degenerative nerve disease; Alzheimer's disease; Parkinson's disease; pyperproliferative disorder; benign dysproliferative disorder; benign dysproliferative disorder; benign dysproliferative disorder; benign sproliferative disorder; benign structural plasticity; screening.
 841 IIDEFPTFVSAKDDSPKLAKEYTDLEVSDKSEIANIQSGADSLPCLELPCDLSFKNIYPK 900
 VTISFRIYKGVIQAIQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRL
 NEATGTKI AYETKVDL VQTSEAI QESLYPTAQLCPSFEEAEATPSPVLPDI VMEAPLNSL
 721 PVDLFSDDSIPEVPQTQEEAVMLMKESLTEVSETVAQHKEERLSASPQELGKPYLESFQP
 DEVHVSDEFSENRSSVSKASISPSNVSALEPQTEMGSIVKSKSLTKEAEKKLPSDTEKED
 LPSAGASVVQPSVSPLEAPPPVSYDSIKLEPENPPPYEEAMNVALKALGTKEGIKEPESF
 SVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLS
 !. .171
/note= "Inhibits NIH 3T3 fibroblast spreading"
 Alternative version of rat neurite growth inhibitor Nogo A.
 site
 /note= "Casein kinase II
 31. .58
/note= "Acidic region"
 NKSVKDAMAKIQAKIPGLKRKAD 360
 AAY71384 standard; protein; 1163 AA
 Location/Qualifiers
 (first entry)

 nhibitory-site
 Modified-site
 02-NOV-2000
 Rattus sp
 1081
 601
 172
 901
 961
 218
 1021
 1141
 172
 172
 172
 278
 338
 AAY71384;
 172
 172
 Region
 AAY71384
XXX AAY71384
XXX AAY
XXX DT 02-1
XXX ABT
XXX ABT
XXX ABT
XXX ABT
XXX ABT
XXX ABT
XXY ABT
XXX ABT
XXX ABT
XXX ABT
XXX ABT
XXX ABT
XXX ABT
XXX ABT
XXX ABT
XXX ABT
XXX ABT
XXX ABT
XXX ABT
XXX ABT
XXX ABT
XXX ABT
XXX ABT
XXX ABT
XXX ABT
XXX ABT
XXX ABT
XXX ABT
XXX ABT
XXX ABT
XXX ABT
XXX ABT
XXX ABT
XXX ABT
XXX ABT
XXX ABT
XXX ABT
XXX ABT
XXX ABT
XXX ABT
XXX ABT
XXX ABT
XXX ABT
XXX ABT
XXX ABT
XXX ABT
XXX ABT
XXX ABT
XXX ABT
XXX ABT
XXX ABT
XXX ABT
XXX ABT
XXX ABT
XXX ABT
XXX ABT
XXX ABT
XXX ABT
XXX ABT
XXX ABT
XXX ABT
XXX ABT
XXX ABT
XXX ABT
XXX ABT
XXX ABT
XXX ABT
XXX ABT
XXX ABT
XXX ABT
XXX ABT
XXX ABT
XXX ABT
XXX ABT
XXX ABT
XXX ABT
XXX ABT
XXX ABT
XXX ABT
XXX ABT
XXX ABT
XXX ABT
XXX ABT
XXX ABT
XXX ABT
XXX ABT
XXX ABT
XXX ABT
XXX ABT
XXX ABT
XXX ABT
XXX ABT
XXX ABT
XXX ABT
XXX ABT
XXX ABT
XXX ABT
XXX ABT
XXX ABT
XXX ABT
XXX ABT
XXX ABT
XXX ABT
XXX ABT
XXX ABT
XXX ABT
XXX ABT
XXX ABT
XXX ABT
XXX ABT
XXX ABT
XXX ABT
XXX ABT
XXX ABT
XXX ABT
XXX ABT
XXX ABT
XXX ABT
XXX ABT
XXX ABT
XXX ABT
XXX ABT
XXX ABT
XXX ABT
XXX ABT
XXX ABT
XXX ABT
XXX ABT
XXX ABT
XXX ABT
XXX ABT
XXX ABT
XXX ABT
XXX ABT
XXX ABT
XXX ABT
XXX ABT
XXX ABT
XXX ABT
XXX ABT
XXX ABT
XXX ABT
XXX ABT
XXX ABT
XXX ABT
XXX ABT
XXX ABT
XXX ABT
XXX ABT
XXX ABT
XXX ABT
XXX ABT
XXX ABT
XXX ABT
XXX ABT
XXX ABT
XXX ABT
XXX ABT
XXX ABT
XXX ABT
XXX ABT
XXX ABT
XXX ABT
XXX ABT
XXX ABT
XXX ABT
XXX ABT
XXX ABT
XXX ABT
XXX ABT
XXX ABT
XXX ABT
XXX ABT
XXX ABT
XXX ABT
XXX ABT
XXX ABT
XXX ABT
XXX ABT
XXX ABT
XXX ABT
XXX ABT
XXX ABT
XXX ABT
XXX ABT
XXX ABT
XXX ABT
XXX ABT
XXX ABT
XXX ABT
XXX ABT
XXX ABT
XXX ABT
XXX ABT
XXX ABT
XXX ABT
XXX ABT
XXX ABT
XXX ABT
XXX ABT
XXX ABT
XXX ABT
XXX ABT
XXX ABT
XXX ABT
XXX ABT
XXX ABT
XXX ABT
XXX ABT
XXX ABT
XXX ABT
XXX ABT
XXX ABT
XXX ABT
XXX ABT
XXX ABT
XXX ABT
XXX ABT
XXX ABT
XXX ABT
XXX ABT
XXX ABT
XXX ABT
XXX ABT
XXX ABT
XXX ABT
XXX ABT
XXX ABT
XXX ABT
XXX ABT
XXX ABT
XXX ABT
XXX ABT
XXX ABT
XXX ABT
XXX ABT
XXX ABT
XXX ABT
XXX ABT
XXX ABT
XXX ABT
XXX ABT
XXX ABT
XXX ABT
XXX ABT
XXX ABT
XXX ABT
XXX ABT
XXX ABT
XXX ABT
XXX
 셤
 ઠે
 g
 ò
 g
 ઠે
 g
 셤
 g
 셤
 g
 g
 셤
 ð
 ò
 ઠે
 δ
 ઠે
 8
 셤
 ð
 ઠે
```

AS

œ

120

9 9 300 171 420

480 171 600 171 99

```
Claim 3; Fig 13; 122pp; English.
 99WO-US026160,
 98US-0107446P.
975. .1162
/note= "Thi
 . .1163
 activity"
 soforms
 Chen MS;
 WPI; 2000-400052/34.
 떠
 (SCHW/) SCHWAB M (CHEN/) CHEN M S.
 Sequence 1163 AA;
 WO200031235-A2
 Modified-site
 Modified-site
 Modified-site
 Modified-site
 Modified-site
 Modified-site
 06-NOV-1998;
 05-NOV-1999;
 02-JUN-2000
 Schwab ME,
 Domain
 Domain
 Region
Region
```

```
PAAGLSAAAVPPAAAAPILDFSSDSVPPAPRGPLPAAPPAAPERQPSWERSPAAPAPSLP 120
 301 AILVENTKEEVIVRSKDKEDLVCSAALHSPQESPVGKEDRVVSPEKTMDIFNEMQMSVVA 360
 481 QIITEKTSPKTSNPFLVAVQDSEADYVTTDTLSKVTEAAVSNMPEGLTPDLVQEACESEL 540
 661 MAAVQETEAPYISIACDLIKETKLSTEPSPDFSNYSEIAKFEKSVPEHAELVEDSSPESE 720
 1 MEDIDQSSLVSSSTDSPPRPPAFKYQFVTBPEDEEBEEBEEBEEBDEDLEBLEVLERK
 181 AASEPVIPSSAEKIMDLMEQPGNTVSSGQEDFPSVLLETAASXPSLSPLSTVSFKEHGYL
 541 NEATGTKIAYETKVDLVQTSEAIQESLYPTAQLCPSFEEAEATPSPVLPDIVMEAPLNSL
 961 RSLSAVLSAELSKTSVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLS
 PAAGLSAAAVPPAAAAPLLDFSSDSVPPAPRGPLPAAPPAAPERQPSWERSPAAPAPSLP
 121 PAAAVLPSKLPEDDEPPARPPPPPAGASPLAEPAAPPSTPAAPKRRGSGSVDETLFALP
 241 GNLSAVSSSEGTIEETLNEASKELPERATNPFVNRDLAEFSELEYSEMGSSFKGSPKGES
 601 LPSAGASVVQPSVSPLEAPPPVSYDSIKLEPENPPPYEEAMNVALKALGTKEGIKEPESF
 721 PVDLFSDDSIPEVPQTQEEAVMLMKESLTEVSETVAQHKEERLSASPQELGKPYLESFQP
 781 NLHSTKDAASNDIPTLTKKEKISLQMEEFNTAIYSNDDLSSSKEDKIKESETFSDSSPIE
 841 IIDEFPTFVSAKDDSPKLAKEYTDLEVSDKSEIANIQSGADSLPCLELPCDLSFKNIYPK
 901 DEVHVSDEFSENRSSVSKASISPSNVSALEPQTEMGSIVKSKSLTKEAEKKLPSDTEKED
 VTISPRIYKGVIQAIQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRL
 MEDIDQSSLVSSSTDSPPRPPAFKYQFVTEPEDEEDEEEEDEEDDEDLEELEVLERK
 361 PVREEYADFKPFEQAWEVKDTYEGSRDVLAARANVESKVDRKCLEDSLEQKSLGKDSEGR
 421 NEDASFPSTPEPVKDSSRAYITCASFTSATESTTANTFPLLEDHTSENXTDEKKIEERKA
 --SVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALLS
 PAAAVLPSKLPEDDEPPARPPPPPAGASPLAEPAAPPSTPAAPKRRGSGS
 61
 172
 61
 121
 172
 172
 172
 172
 172
 172
 g
 В
 셤
 g
 ò
 g
 ò
 q
 ò
 d
 셤
 셤
 g
 셤
 ð
 셤
 ò
 ģ
 ઠે
 g
 Š
 셤
 ò
 g
 ò
 8
 ò
 ઠે
 ò
 ò
 ò
 ò
 The present sequence is an alternative version of rat Nogo A protein which is a potent neural cell growth inhibitor and is free of all central nervous as system (CNS) myelin material with which it is natively associated. Nogo proteins and fragments displaying neurite growth inhibitory activity are used in the treatment of neoplastic disease of the CNS e.g. glioma, plemangioma, medulloblastoma, craniopharyngioma, ependyoma, pinealoma, haemangioblastoma, acoustic neuroma, caliodendroglioma, menagioma, neuroblastoma or retinoblastoma and degenerative nerve diseases e.g. Alzheimar's and Parkinson's diseases.

Therapeutics which promote Nogo activity can be used to treat or prevent hyperproliferative or benign dysproliferative disorders e.g. psoriasis and tissue hypertrophy. Ribozymes or antisense Nogo nucleic acids can be used to inhibit production of Nogo protein to induce regeneration of cauring to not on the process of the CNS in disorders where neurons or to promote structural plasticity of the CNS in disorders where can be used in diagnostic and screening methods for predisposition to disorders and to screen for or test molecules which can maintenance are deficient or desired. The present sequence is an alternative version of the Nogo A sequence shown in Fig. 2A (see AAX71310). SEO ID numbers 35-42 are referred in claim 32 and SEO ID NU. 29 in disclosure of the specification. However the specification of does not include sequences for these SEO ID numbers
 ·O
 Nogo proteins and nucleic acids useful for treating neoplastic disorders of the central nervous system and inducing regeneration of neurons.
 and
 note= "C-terminal common region found in Nogo A, B
"This region is not essential for inhibitory
 95.0%; Score 1732.7; DB 3; Length 1163; 31.0%; Pred. No. 5.7e-61; ive 0; Mismatches 0; Indels 803;
 88. .1023
label= Transmembrane domain
note= "C-terminal hydrophobic region"
 090. .1125
|abel= Transmembrane_domain
note= "C-terminal hydrophobic region"
 site"
 'note= "Protein kinase C (PKC)
 note= "Protein kinase C (PKC)
 note= "Protein kinase C (PKC)
 note= "Protein kinase C (PKC)
 note= "Asn is N-glycosylated'
 note= "Asn is N-glycosylated"
```

1020

277

ij

Gaps

Best Local Similarity 31.0 Matches 360; Conservative

Query Match

900

171

780

```
The invention relates to promoting nerve regeneration or conferring neuroprotection and preventing or inhibiting neuronal degeneration in the central/peripheral nervous system (NS). The method involves administering NS-specific antigen, its analogue or its peptide, a nucleotide sequence the NS-specific antigen or its analogue or combinations. The method is useful for promoting nerve regeneration and preventing neuronal degeneration in central/peripheral nervous system from injury/disease, where the injury is spinal cord injury, blunt crauma, penetrating trauma, hemorrhagic stroke, ischaemic stroke or damages caused by surgery such as tumour excision. The disease is not autoimmune disease or neoplasm. The disease results in a degenerative corresponds or neoplasm. The disease results in a degenerative corresponds or neoplasm. The disease is disease, facial nerve (Bell's) palsy, glaucoma, Huntington's chorea, amyotrophic lateral sclerosis, non-arteritic optic neuropathy, and vitamin deficiency, intervertebral disc herniation, prion diseases such as Creutzfeldt-Jakob disease, carpal tunnel syndrome, peripheral
Nerve regeneration; neuroprotection; neuronal degeneration; CNS; PNS; central nervous system; tranquillizer; Nogo; vulnerary; cerebroprotective; anti-tumour; antidiabetic; anticonvulsant; noctropic; antiparkinsonian; ophthalmological; analgesic; hepatotropic; osteopathic; vasotropic; nephrotropic; cytostatic; antigen; gene therapy;
 the
 Promoting nerve regeneration and preventing neuronal degeneration in central/peripheral nervous system from injury/disease, comprises administering nervous system-specific activated T cells/antigen, or
 to uremia, porphyria, hypoglycemia, Sjorgren Larsson syndrome, acute
 Mosonego
 Beserman P,
 neurotransmitter receptor protein Nogo-A.
 Cohen IR,
 neurotransmitter receptor; rat; receptor
 Example 5; Page 44-47; 93pp; English.
 NKSVKDAMAKIQAKIPGLKRKAD 360
 ABB81074 standard; protein; 1163 AA
 Eisenbach-Schwartz M, Hauben E,
 98IL-00124500.
98WO-US014715.
98US-00218277.
 (YEDA) YEDA RES & DEV CO LTD
 28-JUN-2001; 2001US-00893348.
 99US-00314161
 (first entry)
 WPI; 2002-607255/65.
 Rattus norvegicus
 analogs/peptides.
 N-PSDB; ABN86600
 US2002072493-A1.
 19-MAY-1998;
 21-JUL-1998;
22-DEC-1998;
 19-MAY-1999;
 05-NOV-2002
 13-JUN-2002
 1081
 1141
 ABB81074;
 338
 278
 Moalem
 RESULT 8
ABB 81074
ABB 81074
ABB 81074
ABB 81074
ABB 81074
ABB 81074
ABB 81074
ABB 81074
ABB 81074
ABB 81074
ABB 81074
ABB 81074
ABB 81074
ABB 81074
ABB 81074
ABB 81074
ABB 81074
ABB 81074
ABB 81074
ABB 81074
ABB 81074
ABB 81074
ABB 81074
ABB 81074
ABB 81074
ABB 81074
ABB 81074
ABB 81074
ABB 81074
ABB 81074
ABB 81074
ABB 81074
ABB 81074
ABB 81074
ABB 81074
ABB 81074
ABB 81074
ABB 81074
ABB 81074
ABB 81074
ABB 81074
ABB 81074
ABB 81074
ABB 81074
ABB 81074
ABB 81074
ABB 81074
ABB 81074
ABB 81074
ABB 81074
ABB 81074
ABB 81074
ABB 81074
ABB 81074
ABB 81074
ABB 81074
ABB 81074
ABB 81074
ABB 81074
ABB 81074
ABB 81074
ABB 81074
ABB 81074
ABB 81074
ABB 81074
ABB 81074
ABB 81074
ABB 81074
ABB 81074
ABB 81074
ABB 81074
ABB 81074
ABB 81074
ABB 81074
ABB 81074
ABB 81074
ABB 81074
ABB 81074
ABB 81074
ABB 81074
ABB 81074
ABB 81074
ABB 81074
ABB 81074
ABB 81074
ABB 81074
ABB 81074
ABB 81074
ABB 81074
ABB 81074
ABB 81074
ABB 81074
ABB 81074
ABB 81074
ABB 81074
ABB 81074
ABB 81074
ABB 81074
ABB 81074
ABB 81074
ABB 81074
ABB 81074
ABB 81074
ABB 81074
ABB 81074
ABB 81074
ABB 81074
ABB 81074
ABB 81074
ABB 81074
ABB 81074
ABB 81074
ABB 81074
ABB 81074
ABB 81074
ABB 81074
ABB 81074
ABB 81074
ABB 81074
ABB 81074
ABB 81074
ABB 81074
ABB 81074
ABB 81074
ABB 81074
ABB 81074
ABB 81074
ABB 81074
ABB 81074
ABB 81074
ABB 81074
ABB 81074
ABB 81074
ABB 81074
ABB 81074
ABB 81074
ABB 81074
ABB 81074
ABB 81074
ABB 81074
ABB 81074
ABB 81074
ABB 81074
ABB 81074
ABB 81074
ABB 81074
ABB 81074
ABB 81074
ABB 81074
ABB 81074
ABB 81074
ABB 81074
ABB 81074
ABB 81074
ABB 81074
ABB 81074
ABB 81074
ABB 81074
ABB 81074
ABB 81074
ABB 81074
ABB 81074
ABB 81074
ABB 81074
ABB 81074
ABB 81074
ABB 81074
ABB 81074
ABB 81074
ABB 81074
ABB 81074
ABB 81074
ABB 81074
ABB 81074
ABB 81074
ABB 81074
ABB 81074
ABB 81074
ABB 81074
ABB 81074
ABB 81074
ABB 81074
ABB 81074
ABB 81074
ABB 81074
ABB 81074
ABB 81074
ABB 81074
ABB 81074
ABB 81074
ABB 81074
ABB 81074
ABB 81074
ABB 81074
ABB 81074
ABB 81074
ABB 81074
ABB 81074
ABB 81074
ABB 81074
ABB 81074
ABB 81074
ABB 81074
ABB 810
 g
 셤
 ò
 ò
```

```
sensory neuropathy, chronic ataxic neuropathy, biliary cirrhosis, primary amyloidosis, obstructive lung diseases, acromegaly, malabsorption syndromes, polycythemia vera, immunoglobulin (1g)A- and 1gG gamma-pathies, complications of various drugs (e.g., metronidazole) and toxins (e.g., alcohol or organophosphates), Charcot-Marie-Tooth disease, ataxia adrenomycloneuropathy, Giant axonal neuropathy, Refoun's disease, Fabry's disease, or lipoproteinemia. The present sequence represents the rat neurotransmitter receptor protein Nogo-A, an example of NS-specific
 120
 420
 171
 9
 720
 171
 780
 171
 171
 421 NEDASFPSTPEPVKDSSRAYITCASFTSATESTTANTFPLLEDHTSENKTDEKKIEERKA 480
 481 QIITEKTSPKTSNPFLVAVQDSEADYVTTDTLSKVTEAAVSNMPEGLTPDLVQEACESEL 540
 541 NEATGTKIAYETKVDLVQTSEAIQESLYPTAQLCPSFEEAEATPSPVLPDIVMEAPLNSL 600
 181 AASEPVIPSSAEKIMDLMEQPGNTVSSGQEDFPSVLLETAASLPSLSPLSTVSFKEHGYL 240
 301 AILVENTKEEVIVRSKDKEDLVCSAALHSPQESPVGKEDRVVSPEKTMDIFNEMQMSVVA 360
 9
 661 NAAVQETEAPYISIACDLIKETKLSTEPSPDFSNYSEIAKFEKSVPEHAELVEDSSPESE
 781 NLHSTKDAASNDIPTLTKKEKISLQMEEFNTAIYSNDDLLSSKEDKIKESETFSDSSPIE
 PAAGLSAAAVPPAAAAPLIDFSSDSVPPAPRGPLPAAPPAAPERQPSWERSPAAPAPSLP
 601 LPSAGASVVQPSVSPLEAPPVSYDSIKLEPENPPPYEEAMNVALKALGTKEGIKEPESF
 721 PVDLFSDDSIPEVPQTQEEAVMLMKESLTEVSETVAQHKEERLSASPQELGKPYLESFQP
 1 MEDIDOSSLVSSSTDSPPRPPAPKYOFVTEPEDEEDEEDEEDEEDDEDLEELEVLERK
 PAAGLSAAAVPPAAAAPLLDFSSDSVPPAPRGPLPAAPPAAPERQPSWERSPAAPAPSLP
 241 GNLSAVSSSEGTIEETLNEASKELPERATNPFVNRDLAEFSELEYSEMGSSFKGSPKGES
 PAAAVLPSKLPEDDEPPARPPPPAGASPLAEPAAPPSTPAAPKRRGSGS-----
 361 PVREEYADFKPFEQAWEVKDTYEGSRDVLAARANVESKVDRKCLEDSLEQKSLGKDSEGR
 Gaps
 Length 1163;
 803;
 Score 1732.7; DB 5; Length
Pred. No. 5.7e-61;
0; Mismatches 0; Indels
 95.0%;
31.0%;
 Conservative
 Similarity
 Sequence 1163 AA;
 Best Local Sim:
Matches 360;
 61
 121
 172
 61
 172
 172
 172
 172
 172
 172
 Query Match
 antigen
 888888888888888
 g
 셤
 원
 셤
 g
 8 8
 셤
 à
 셤
 ò
 g
 ò
 g
 ઠે
 В
 à
 요
 ò
 셤
 ò
 a
 8
 ઠ
 ò
 8
 ð
 ઠે
```

| DD 1 MEDIDQSSLVSSTDSPPRPPAFKYQFVTEPEDEEEEEEEEEEDEEUDEDLEELEVLERK 60 | Oy 61 PAAGLSAAAVPPAAAAPLLDFSSDSVPPAPRGPLPAAPPAAPERQPSWERSPAAPAPSLP 120 | Db 61 PAAGLSAAAVPPAAAAPLLDFSSDSVPPAPRGPLPAAPPAAPERQPSWERSPAAPAPAPALD 120 | Qy 121 PAANVLPSKLPEDDEPPARPPPPAGASPLAEPAAPPSTPAAPKRGSGS 171          |                                                  | ογ 172 171                                                         | Db 181 AASEPVIPSSAEKIMDLMEQPGNTVSSGQEDFPSVLLETAASLPSLSPLSTVSFKEHGYL 240 Qy 172 | Db 241 GNLSAVSSSEGTIEETLNEASKELPERATNPFVNRDLAEFSELEYSEMGSSFKGSPKGES 300 | Qy 172 171 | Db 301 AILVENTKEEVIVRSKDKEDLVCSAALHSPQESPVGKEDRVVSPEKTMDIFNEMQMSVVA 360 | 172  | DD 361 PVREEYADFKFFEQAWEVKDTYEGSRDVLAARANVESKVDRKCLEDSLEQKSLGKDSEGR 420<br>CC. 177 | 421 NEDASFPSTPEPVKDSSRAYITCASFTSATESITANTFPLLEDHISRNKTDEKKIERBKA |           | 481 OTTTEKTSPKTSNPFLVAVONSFADYVTTPTLSKVTRAAVSNMPEGLTPDLVOBACESEL |                               | OY 1/2                                                           | יייי איייי  1/1              | UD OUI DESAGASVVQESVSEUBAFFEVSIDSIANDEFBNEFFIBBANNVANAAAAAAAAAAEBST 0000 | 112<br>661 NAAVOEMPADVICIACH, IKEMYI, CHEDGDDGGNYCRIAKEPKGVDEHARI VENGGDEGR | 172                           | 721 PVDLFSDDSIPEVPOTOFFAVMLMKRSLTRVSGTVAOHKEERLSASPOELGKPYLESFOP | 271                  | 781 NIHSTKDAASNDIDTIJTKKEKISLOMERBNTAIVSNDDIJSSKEDKIKESETPSDSSPIR | 172                                                                                                                                                                                     | 841 IIDEFPTFVSAKDDSPKLAKEYTDLEVSDKSEIANIQSGADSLPCLELPCDLSFKNIYPK | 172                                                                   | Db 901 DEVHVSDEFSENRSSVSKASISPSNVSALEPQTEMGSIVKSKSLTKEAEKKLPSDTEKED 960  Qy 172SVVDLLYWRDIKKTGVYFGASLFLLLSLTVFSIVSVTAYIALALLS 217                                                            | Db 961 RSLSAVLSAELSKTSVVDLLYWRDIKKTGVVFGASLFLLISLTVFSIVSYTAYIALALLS 1020 | Oy 218 VTISFRIYKGVIQALQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRL 277 | Qy 278 FLVDDLVDSLKFAVLMWVFTYVGALFNGLTLLILALISLFSIPVIYERHQVQIDHYLGLA 337                                            | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 172 171                                                             | 841 IIDEFPTFVSAKDDSPKLAKEYTDLEVSDKSEIANIQSGADSLPCLELPCDLSFKNIYPK 900   | 172 171                                                                  | 901 DEVHVSDEFSENRSSVSKASISPSNVSALEPQTEMGSIVKSKSLTKEAEKKLPSDTEKED 960 | SUVDLLYWRDIKKTGVVFGASLFLILSLTVFSIVSVTAYIALIS 217 | RSLSAVLSABLSKTSVVDLLYWRDIKKTGVVFGASLFILLLSLTVFSIVSVTAYIALALLS 1020 | 218 VTISFRIYKGVIQAIQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRL 277           | YLGLA 337                                                               | 1140       | NKSVKDAMAKIQAKIPQLKRKAD 360                                             | 1163 | NESULT 9 AD026199                                                                  | 26399 standard; protein; 1163 AA.                                | ADO26399; | 29-JUL-2004 (first entry)                                        | Rat truncated Nogo-A protein. | rat; human; Nogo-A; truncated; affinity; membrane-bound protein. | Rattus sp.                                                                                                      | WO2004039836-A1. | 13-MAY-2004.                                                             | 31-OCT-2002; 2002WO-EP012210.                                               | 31-OCT-2002; 2002MO-BP012210. | (PIER-) PIERIS PROTEOLAB AG.                                     | Skerra A, Fiedler M; | WPI; 2004-376159/35.                                              | New isolated truncated Nogo-A polypeptide that corresponds to a truncated form of the Nogo-A protein, useful for identifying a compound having detectable affinity to a Nogo-A protein. | Claim 1; Fig 6A; 80pp; English.                                  | present invention relates to an isolated truncated Nogo-A polypeptide | responds to a truncated form of the Nogo-A protein from the rat the human. The truncated polypeptide is useful for identifying a having detectable affility to a Nogo-A protein. The present |                                                                          | 95.0%; Score 1732.7; DB 8; Length 1163;<br>y 31.0%; Pred. No. 5.7e-61;  | 350; CONSELVATIVE U; MIBMATCHES U; INCELE 803; GADS 1; I MEDIDQSSLVSSTUSPPRPPAFKYQFVTEPEDEEDEEEEEDDEEDEELEVLERK 60 |

원

ઠે

```
1080
 961 RSLSAVLSAELSKTSVVDLLYWRDIKKTGVVFGASLFĻLLSLTVFSIVSYTAYIALALLS 1020
 780
 171
 VTISFRIYKGVIQAIQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRL 277
 FLVDDLVDSLKFAVLMWVFTYVGALFNGLTLLILALISLFSIPVIYERHQVQIDHYLGLA 337
 301 AILVENTKEEVIVRSKDKEDLVCSAALHSPQESPVGKEDRVVSPEKTMDIFNEMQMSVVA 360
 540
 171
 171
 781 NLHSTKDAASNDIPTLTKKEKISLQMEEFNTAIYSNDDLLSSKEDKIKESETFSDSSPIE 840
 180
 241 GNLSAVSSSEGTIBETLNEASKELPERATNPFVNRDLAEFSELEYSEMGSSFKGSPKGES 300
 361 PVREEYADFKPFEQAWEVKDTYEGSRDVLAARANVESKVDRKCLEDSLEQKSLGKDSEGR 420
 421 NEDASFPSTPEPVKDSSRAYITCASFTSATESTTANTFPLLEDHTSENKTDEKKIEERKA 480
 541 NEATGTKIAYETKVDLVQTSEAIQESLYPTAQLCPSFEEAEATPSPVLPDIVMEAPLNSL 600
 171 ---
 661 NAAVQETEAPYISIACDLIKETKLSTEPSPDFSNYSEIAKFEKSVPEHAELVEDSSPESE 720
 841 IIDEPPTFVSAKODSPKLAKEYTDLEVSDKSEIANIQSGADSLPCLELPCDLSFKNIYPK 900
 901 DEVHVSDEFSENRSSVSKASISPSNVSALEPQTEMGSIVKSKSLTKEABKKLPSDTEKED 960
 VTISFRIYKGVIQAIQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRL
 721 PVDLFSDDSIPEVPQTQEEAVMLMKESLTEVSETVAQHKEERLSASPQELGKPYLESFQP
 181 AASEPVIPSSAEKIMDLMEQPGNTVSSGQEDFPSVLLETAASLPSLSPLSTVSFKEHGYL
 481 QIITEKTSPKTSNPFLVAVQDSEADYVTTDTLSKVTEAAVSNMPEGLTPDLVQEACESEL
 601 LPSAGASVVQPSVSPLEAPPPVSYDSIKLEPENPPPYEEAMNVALKALGTKEGIKEPESF
 -----SVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALLS
PAAAVLPSKLPEDDEPPARPPPPAGASPLAEPAAPPSTPAAPKRRGSGS
 NKSVKDAMAKIQAKIPGLKRKAD 360
 1021
 1141
 121
 172
 1081
 172
 172
 172
 172
 172
 278
 338
 172
 172
 172
 172
 172
 172
121
 172
 셤
 8
 d
 à
 요
 셤
 셤
 셤
 ò
 엄
 ઠે
 g
 ઠે
 셤
 ò
 g
 ઠે
 g
 ò
 엄
 ⋧
 ద
 ઠે
 g
 ò
 a
 8
 유
 ò
 à
 ઠે
 δ
 ठे
 The present invention describes a binding molecule which binds to human NogoA polypeptide, human NiG, human NiG-D20 or human NogoA 623-640 with a dissociation constant of less than 1000nM. Also described: (1) a polynucleotide encoding the binding molecule; (2) an expression vector or system comprising the polynucleotide; (3) a host cell comprising the binding molecule and a carrier or diluent; and (5) treating the binding molecule and a carrier or diluent; and (5) treating diseases associated with nerve repair. The binding molecule has neuroprotective activity, and can be used in gene therapy. The binding molecule is useful in preparing a composition for treating central nervous system (CNS) injury or neurodegenerative disorders. The present sequence represents rat NogoA, which is used in the exemplification of the present invention.
 New binding molecule that binds to the human NogoA polypeptide, NiG, NiG-
D20 or NogoA623-640, useful in preparing a composition for treating CNS
injury or neurodegenerative disorders.
 61 PAAGLSAAAVPPAAAAPLLDFSSDSVPPAPRGPLPAAPPAAPERQPSWERSPAAPAPSLP 120
 120
 9
 9
 binding molecule; human; NogoA; NiG; NiG-D20; NogoA_623-640;
nerve repair; neuroprotective; gene therapy;
central nervous system injury; CNS injury; neurodegenerative disorder;
 1 MEDIDQSSLVSSSTDSPPRPPPAFKYQFVTEPEDEEBEBEBEBEBDBEDLEBLEVLERK
 61 PAAGLSAAAVPPAAAAPLLDFSSDSVPPAPRGPLPAAPPAAPERQPSWERSPAAPASLP
 MEDIDQSSLVSSSTDSPPRPPPAFKYQFVTEPEDEEDEEEEEDEEEDDEDLEELEVLERK
 Gaps
 Vitaliti A;
 0; Indels 803;
 DB 8; Length 1163;
 Schnell L, Schwab ME,
 95.0%; Score 1732.7; DB 8 31.0%; Pred. No. 5.7e-61;
 0; Mismatches
 Example 1; SEQ ID NO 26; 121pp; English.
 NKSVKDAMAKIQAKIPGLKRKAD 360
 Ź
 ADP45572 standard; protein; 1163
 NogoA protein SEQ ID NO:26.
 Mir AK, Oertle T,
 09-DEC-2003; 2003WO-EP013960.
 10-DEC-2002; 2002GB-00028832.
 (NOVS) NOVARTIS AG.
(NOVS) NOVARTIS PHARMA GMBH.
(UYZU-) UNIV ZUERICH.
 09-SEP-2004 (first entry)
 Matches 360; Conservative
 WPI; 2004-468818/44.
 Local Similarity
 Rattus norvegicus.
 Sequence 1163 AA;
 N-PSDB; ADP45571.
 WO2004052932-A2.
 24-JUN-2004
 Barske C,
Zurini M;
 1141
 ADP45572;
 Query Match
338
 Rat
```

ઠ 유 ઠ 셤 Length 1162;

DB 3;

Score 1726.7;

94.78; 30.9%;

Similarity

Query Match

```
Rat; neurite growth inhibitor; Nogo A; neural cell; myelin; CNS; central nervous system; neoplastic disease; antiproliferative; glioma; natisense gene therapy; neuroblastoma; menagioma; retinoblastoma; degenerative nerve disease; Alzheimer's disease; Parkinson's disease; hyperproliferative disorder; benign dysproliferative disorder; diagnosis; psoriasis; tissue hypertrophy; neuronal regeneration; treatment; structural plasticity; screening; mutant; mutein.
 Nogo A truncated protein used in the construction of mutant Nogo-A.
 AAY71557 standard; protein; 1162 AA
 99WO-US026160
 06-NOV-1998; 98US-0107446P
 02-NOV-2000 (first entry)
 Chen MS;
 WPI; 2000-400052/34
 (SCHW/) SCHWAB M E. (CHEN/) CHEN M S.
 WO200031235-A2
 05-NOV-1999;
 02-JUN-2000
 Schwab ME,
 Rattus sp.
 AAY71557;
RESULT 11
AAY71557
```

Nogo proteins and nucleic acids useful for treating neoplastic disorders of the central nervous system and inducing regeneration of neurons.

Example; Page; 122pp; English.

The patent relates to neurite growth inhibitor Nogo which is free of all central nervous system (CNS) myelin material with which it is natively central nervous system (CNS) myelin material with which it is natively central nervous system (CNS) myelin material with which it is natively inhibitory activity are used in the treatment of neoplastic disease of the CNS e.g. glioma, haemangloblastoma, acoustic neuroma, capingma, planaloma, haemangloblastoma or retinoblastoma, and espendyoma, plinealoma, neuroblastoma or retinoblastoma and degenerative nerve diseases e.g. Alzheimer's and Parkinson's diseases.

CN forzapeutics which promote Nogo activity can be used to treat or prevent hyperproliferative or benign dysproliferative disorders e.g. psoriasis and tissue hypertrophy. Ribozymes or antisense Nogo nucleic acids can be used to inhibit production of Nogo protein to induce regeneration of neurons or to promote structural plasticity of the CNS in disorders where constructing growth, regeneration or maintenance are deficient or desired. The neurite growth, regeneration or maintenance are deficient or desired. The animal models can be used in diagnostic and screening methods for treat or prevent disorders or diseases of the CNS. The present sequence for most form of rat Nogo A protein shown in AAY1310, which is used for mapping the inhibitory sites of Nogo protein. Major inhibitory cased for mapping the inhibitory sites of Nogo protein. Major inhibitory to NIH 373 fibroblast spreading. Note: The was found to be inhibitory to NIH 373 fibroblast spreading. Note: The was found to be inhibitory to NIH 373 fibroblast spreading. Note: The was found to be inhibitory to NIH 373 fibroblast spreading. Note: The wood A sequence shown in AAY1310. SEQ ID numbers 35-42 are referred in claim 32 and SEQ ID NO: 29 in disclosure of the specification.

Sequence 1162 AA;

```
1;
 1020
 217
 120
 120
 171
 171
 181 AASEPVIPSSAEKIMDLMEQPGNTVSSGQEDFPSVLLETAASLPSLSPLSTVSFKEHGYL 240
 171
 420
 171
 480
 171
 171
 999
 171
 720
 780
 171
 840
 900
 171
 241 GNLSAVSSSEGTIEETLNEASKELPERATNPFVNRDLAEFSELEYSEMGSSFKGSPKGES 300
 301 AILVENTKEEVIVRSKDKEDLVCSAALHSPQESPVGKEDRVVSPEKTMDIFNEMQMSVVA 360
 541 NEATGTKIAYETKVDLVQTSEAIQESLYPTAQLCPSFEEAEATPSPVLPDIVMEAPLNSL 600
 218 VTISFRIYKGVIQAIQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRL 277
 9
 9
 1 MEDIDQSSLVSSSTDSPPRPPPAFKYQFVTEPEDEEBEEEEDEEEDDEDLEELEVLERK
 PAAGLSAAAVPPAAAAPLIDFSSDSVPPAPRGPLPAAPPAAPERQPSWERSPAAPAPSLP
 PAAAVLPSKLPEDDEPPARPPPPPPAGASPLAEPAAPPSTPAAPKRRGSGS-----
 561 NAAVQETEAPYISIACDLIKETKLSTEPSPDFSNYSEIAKFEKSVPEHAELVEDSSPESE
 PAAGLSAAAVPPAAAAPLLDFSSDSVPPAPRGPLPAAPPAAPERQPSWERSPAAPAPSLP
 361 PVREEYADFKPFEQAWEVKDTYEGSRDVLAARANVESKVDRKCIEDSLEQKSLGKDSEGR
 121 NEDASFPSTPEPVKDSSRAYITCASFTSATESTTANTFPLLEDHTSENKTDEKKIEERKA
 501 LPSAGASVVQPSVSPLEAPPPVSYDSIKLEPENPPPYEEAMNVALKALGTKEGIKEPESF
 721 PVDLFSDDSIPEVPQTQEEAVMLMKESLTEVSETVAQHKEERLSASPQELGKPYLESFQP
 781 NLHSTKDAASNDIPTLTKKEKISLQMEEFNTAIYSNDDLLSSKEDKIKESETFSDSSPIE
 341 IIDEFPTFVSAKDDSPKLAKEYTDLEVSDKSEIANIQSGADSLPCLELPCDLSFKNIYPK
 901 DEVHVSDEFSENRSSVSKASISPSNVSALEPQTEMGSIVKSKSLTKEAEKKLPSDTEKED
 961 RSLSAVLSAELSKTSVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLS
 1 MEDIDQSSLVSSSTDSPPRPPARKYQFVTEPEDEEDEEEEEBDEEDDEDLEELEVLERK
 481 QIITEKTSPKTSNPFLVAVQDSEADYVTTDTLSKVTEAAVSNMPEGLTPDLVQEACESEL
 -----SVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLS
 Gaps
 803;
 Indels
 ,
0
Pred. No. 1e-60;
0; Mismatches
 359; Conservative
 61
 121
 61
 172
 172
 172
Best Local
Matches 35
 8
 g
 8
 a
 δ
 g
 셤
 셤
 g
 g
 à
 g
 ઠે
 g
 g
 원
 g
 a
 ò
 ò
 ò
 8
 ò
 요
 õ
 ò
 ò
 8
 ò
 g
 ò
 쉽
 ð
```

| 60 PAAGLSAAPVPP-AAAPLLDFSSDSVPPAPRGPLPAAPPTAPERQPSWERSPAASAPSLP 118 121 PAAAVLPSKLPEDDEPPARPPPPPAGASPLAEPAAPPSTPAAPKRRGSGS 171 119 PAAAVLPSKLPEDDEPPARPPPPPAGASPLAEPAAPPSTPAAPKRRGSGSVDETLFALP 176 172 | GNLSAVASTEGTIEETLNEASRELPERATNPFVNRESAEFSVLEYSEMGSSFNGSPKGES    | AML/JENTIKEEVIVRSKDKEDLVCSAALHNPQESPATLTKVVKEDGVMSPEKTMDIFNEMK | 172 171                            | 357 MSVVAPVREEYADFKPFEQAWEVKDTYEGSRDVLAARANMESKVDKKCFEDSLEQKGHGK 416 | 172 171 417 DSESRNENASFPRTPELVKDGSRAYITCDSFSSATESTAANIFPVLEDHTSENKTDEKKI 476                    | 172 171                                   | EERKAQIITEKTSPKTSNPPLVAIHDSEADYVTTDNLSKVTEAVVATMPEGLTPDLVQEA |                                        | 537 CESSELNEATGIKLAYETKVDLVQISEAIQESIXPIAQLCFSFEKAKAIFSFVLFDIVMEA 596      | 597 PLNSLLPSTGASVAQPSASPLEVPSPVSYDGIKLEPENPPPYEEAMSVALKTSDSKEEIK 656 |         | 172                                             | SPESEFVDLFSDDSIPEVPQTQEEAVMLMKESLTEVSETVTQHKHKERLSASPQEVGKPY                                                                           | 172 |                                               | DSSPIEIIDEFPTFVSAKDDSPKEYTDLEVSNKSEIANVQSGANSLPCSELPCDLSFKNT |                                                                                                                                                                                                                                   | YPKDEAHVSDEFSKSRSSVSKVPLLLPNVSALESQI EMGNI VKPKVLTKEAEEKLPSDTE | 1/2 | 215 LLSVTISFRIYKGVIOAIOKSDEGHPFRAYLESEVAISEELVOKYSNSALGHVNSTIKEL 274 |                                                                                                                                                                  | 275 RRLPLVDDLVDSLKPAVLMMVFTYVGALFNGLTLLILALISLFSIPVIYERHQVQIDHYL 334 | 335 GLANKSVKDAMAKIQAKIPGLKRKAD 360<br>                                                                                                       |    |
|--------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|-----------------------------------------------------------------|----------------------------------------------------------------|------------------------------------|----------------------------------------------------------------------|-------------------------------------------------------------------------------------------------|-------------------------------------------|--------------------------------------------------------------|----------------------------------------|----------------------------------------------------------------------------|----------------------------------------------------------------------|---------|-------------------------------------------------|----------------------------------------------------------------------------------------------------------------------------------------|-----|-----------------------------------------------|--------------------------------------------------------------|-----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|----------------------------------------------------------------|-----|----------------------------------------------------------------------|------------------------------------------------------------------------------------------------------------------------------------------------------------------|----------------------------------------------------------------------|----------------------------------------------------------------------------------------------------------------------------------------------|----|
| 3 6 6 6 6                                                                                                                                                                                              | ž A ž                                                           | A 4                                                            | ò                                  | q                                                                    | & g                                                                                             | ò                                         | qq                                                           | à à                                    | g &                                                                        | qq                                                                   | ò       | 3 &                                             | qq                                                                                                                                     | ò € | 3 8                                           | 전<br>전                                                       | ò                                                                                                                                                                                                                                 | ብ (                                                            | 충 옵 | ð                                                                    | g q                                                                                                                                                              | රු අ                                                                 | & g                                                                                                                                          | .* |
| Db 1021 VTISFRIYKGVIQAIQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRL 1080  Qy 278 FLVDDLVDSLKFAVLMWVFTYVGALFNGLTLLILALISLFSIPVIYERHQVQIDHYLGLA 337                                                     | RESULT 12<br>ADT09537<br>ID ADT80537 standard: protein: 1162 AA | ADT89537;                                                      | AA 16-DEC-2004 (first entry)<br>XX | Mus musculue                                                         | KW Nerve regeneration, gene therapy, vaccine, neuroprotective, nootropic,<br>KW Nogo; mouse. XX | OS Mus musculus.<br>XX PN US2004191240-A1 |                                                              | XX<br>PF 31-JUL-2003; 2003US-00633423. | AX<br>PR 28-MAR-2003; 2003JP-00092923.<br>PR 30-APR-2003; 2003US-00427741. | XX XX TOHY/) TOHYAMA M. PA (YAMA) YAMASHITA T.                       | Тоћуаша | DR WPI; 2004-698659/68.<br>DR N-PSDB; ADT89536. | Regenerating nerves or modulating nerve regeneration comprises inhibi or modulating p75 signal transduction pathway by administering a |     | P.S. Example 2; SEQ ID NO 10; 209pp; English. |                                                              | CC modulating a p/s signal transduction paraway. The invention is useful for CC treating, preventing or diagnosing neurological diseases based on nerve CC regeneration and for identifying agents useful for nerve regeneration. |                                                                |     | SQ Sequence 1162 AA;                                                 | Query Match 89.8%; Score 1637; DB 8; Length 1162; Best Local Similarity 29.8%; Pred. No. 4.2e-57; Matches 348; Conservative 2; Mismatches 6; Indels 810; Gaps 4; | 1 MEDIDQSSLVSSSTDSPPRPPAFKYQFVTEPEDEEDEEBEEBDEEDEELEVLERK 60         | DD 1 MEDIDQSSLVSSSADSPPRPPPAFKYQFVTEPEDEEDEEDEE-EEEDDEDLEELEVLERK 59  Qy 61 PAAGLSAAAVPPAAAAPLLDFSSDSVPPAFRGPLFAAPPAAPERQPSWERSPAAFAPSLP 120 |    |

```
g
 g
 q
 g
 qq
 셤
 g
 8
 ઠે
 셤
 ò
 à
 ò
 셤
 ò
 g
 à
 ద
 ò
 q
 ò
 g
 ò
 g
 ò
 ò
 셤
 ò
 Š
 ò
 ò
 The invention relates to a method of identifying compounds that influence fat cell number or size comprising providing a cell that expresses a gene and an agent, exposing the cell to the agent and identifying fat cell number or size relative to cells not exposed to the agent. The method also comprises providing an expression vector and an agent, exposing the vector to the agent, detecting a change in expression of the gene relative to expression of the gene in an expression of the gene control of the agent, treating a subject with the agent and identifying fat cell number or size in the subject with the agent comprises an antistense chigonucleotide. The subject comprises a manual, preferably a human. The method also comprises providing a polypeptide and an agent, exposing the polypeptide to the agent, detecting binding of the agent to the subject with the agent and identifying fat cell number or size in the subject. The agent and identifying fat cell number or size in the subject. The agent and identifying the method of regulating fat cell number or size in the subject. The agent and identifying the method of regulating fat cell number or size in the subject. The agent and adentifying the method of regulating fat cell number or size in the subject. The agent comprises an antibody, A method of regulating fat cell number or size in the subject. The agent and identifying the method of regulating fat cell number or size in the subject.
 Identifying compounds that influence fat cell number or size for treating or preventing obesity or diabetes by exposing the cell to the agent and identifying fat cell number or size relative to cells not exposed to the
 number or size comprises providing a subject containing fat cells and an agent that changes the expression of a gene, and treating the subject with the agent under conditions so that fat cell size or number in the subject is altered. The method is useful for identifying compounds that
 influence fat cell number or size, for preparing a composition for treating or preventing obesity or diabetes. This sequence represents a mouse polypeptide used in the scope of the invention.
 Mouse; fat cell number; fat cell size; obesity; diabetes; anorectic;
 89.0%; Score 1622.9; DB 8; Length 1163; 29.7%; Pred. No. 1.6e-56; ive 2; Mismatches 7; Indels 811;
 Claim 14; SEQ ID NO 431; 275pp; English.
 AD008105 standard; protein; 1163 AA
 09-OCT-2002; 2002US-00267502.
 09-OCT-2002; 2002US-00267502
 Mouse polypeptide #57
 (LIFE-) LIFE SCI DEV
 WPI; 2004-328526/30.
N-PSDB; ADO07888.
 al Similarity
347; Conser
 Kim J, Galant R;
 Sequence 1163 AA;
 US2004071700-A1.
 antidiabetic
 01-JUL-2004
 15-APR-2004
 ADO08105;
 Query Match
 Local
 Mus sp.
 Best Loca
Matches
RESULT 13
 AD008105
```

PAAGLSAAAVPPAAAAPLLDFSSDSVPPAPRGPLPAAPPAAPERQPSWERSPAAPAPSLP 120

MEDIDÓSSLVSSSADSPPRPPAFKYOFVTEPEDEEDEEDEE-EEEDDEDLEELEVLERK 1 MEDIDQSSLVSSSTDSPPRPPAFKYQFVTEPEDEEDEEEEEDEEEDDEDLEELEVLERK

> g ò,

ઠે

Conservative

```
1076
 273
 926
 213
 716
 717 SPESEPVDLFSDDSIPEVPOTQEEAVMLMKESLTEVSETVTOHKHKERLSASPQEVGKPY 776
 171
 297 AMLVENTKEEVIVRSKDKEDLVCSAALHNPQESPATLTKVVKEDGVMSPEKTMDIFNEMK 356
 357 MSVVAPVREEYADFKPFEQAWEVKDTYEGSRDVLAARANMESKVDKKCFEDSLEQKSHGK 416
 337 DSGPIEIIDEFPTFVSAKDDSPKEYTDLEVSNKSEIANVOSGANSLPCSELPCDLSFKNT 896
119 PAAAVLPSKLPEDDEPPAR--PPAPAGASPLAEPAAPPSTPAAPKRGSGSVDETLFALP
 777 LESFQPNLHITKDAASNEIPTLTKKETISLQMEEFNTAIYSNDDLLSSKEDKMKESETFS
 177 AASEPVIPSSAEKIMDLKEQPGNTVSSGQEDFPSVLFETAASLPSLSPLSTVSFKEHGYL
 237 GNLSAVASTEGTILEETLNEASRELPERATNPFVNRESAEFSVLEYSEMGSSFNGSPKGES
 417 DSESRNENASFPSTPELVKDGSRAYITCDSFTSATESTAANIFPVLEDHTSENKTDEKKI
 597 PLNSLLPSTGASVAQPSASPLEVPSPVSYDGIKLEPENPPPYEEAMSVALKTSDAKEEIK
 557 EPESFNAAAQEAEAPYISIACDLIKETKLSTEPSPGFSNYSEIAKFEKSVPDHCELVDDS
 997 YPKDEAHVSDEFSKSRSSVSKVPLLLPNVSALESQIEMGNIVKPKVLTKEAEEKLPSDTE
 --SVVDLLYWRDIKKTGVV-FGASLFLLLSLTVFSIVSVTAYIAL
 ALLSVTISFRIYKGVIQAIQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKE
 LRRLFLVDDLVDSLKFAVLMWVFTYVGALFNGLTLLILALISLFSIPVIYERHQVQIDHY
 477 EERKAQIITEKTSPKTSNPFLVAIHDSEADYVTTDNLSKVTEAVVATMPEGLTPDLVQEA
 337 CESELNEATGTKIAYETKVDLVQTSEAIQESIYPTAQLCPSFEEAEATPSPVLPDIVMEA
 PAAAVLPSKLPEDDEPPARPPPPPAGASPLAEPAAPPSTPAAPKRGSGS
 LGLANKSVKDAMAKIQAKIPGLKRKAD 360
 334
 172
 214
 274
 172
 172
 172
 172
 g
 Š
 ò
```

```
Sequence 373 AA;
 8
 셤
 ઠે
 셤
 δ
 셤
 ò
 셤
 ઠે
 셤
 ò
 g
 ઠે
 셤
 AAY5362-43 represent bone marrow secreted proteins of human bone marrow stromal cells. The proteins can exhibit cytokine, cell proliferation, or cell differentiation activity (either inducing or inhibiting). They can be used to support colony forming cells or factor-dependent cell lines, to regulate hematopoiesis, and to treat myeloid or lymphoid cell lines, proliferation of erythroid progenitor cells, and to treat various anemias. They can have colony simulating factor (CSP) activity and can be used to support the growth and proliferation of myeloid cells such as granulocytes, monocytes or macrophages, to prevent or treat myelo.

Suppression, to support the growth and proliferation of megakaryocytes and platelets, thereby allowing prevention or treatment of platelet disorders such as thrombocytopenia, to support the growth and proliferation of megakaryocytes and platelets, thereby allowing prevention or treatment of platelet compartment stem cells, either in place of or in conjunction with platelet transfusions, to treat stem cell disorders, such as aplastic anaemia and paroxysmal nocturnal hemoglobinuria, or to reconjunction or the stem cells compartment after irradiation or chemotherapy.
 Bone marrow secreted protein, bone marrow stromal cell; cytokine; cell proliferation; cell differentiation; hematopoiesis; anaemia; myeloid cell deficiency; lymphoid cell deficiency; myeloid cell; merythroid progenitor cell; colony stimulating factor; granulocyte; monocyte; macrophage; myelo-suppression; megakaryocyte; platelet disorder; thrombocytopenia; hematopoeitic stem cell; stem cell disorder; aplastic anaemia; bone differentiation; paroxysmal nocturnal hemoglobinuria; bone growth; cartilage; tendon; bone fracture; cartilage damage; artificial joint.
 New isolated human polynucleotide and secreted proteins can induce production of other cytokines in certain cell populations.
 A bone marrow secreted protein designated BMS112
1137 LGLANKSVKDAMAKIQAKIPGLKRKAE 1163
 Claim 2; Page 74; 120pp; English
 AAY53624 standard; protein; 373
 98US-0101603P.
98US-0102540P.
 98WO-US027008
 97US-0068958P
 (first entry)
 2000-038344/03.
 (CHIR) CHIRON CORP.
 N-PSDB; AAZ36230
 Cao L;
 22-FEB-2000
 Homo sapiens
 WO9933979-A2
 18-DEC-1998;
 30-DEC-1997;
 30-SEP-1998;
 24-SEP-1998;
 08-JUL-1999
 AAY53624;
 Lin H,
 RESULT 14
 AAYS 3624

THE PART OF THE PAR
셤
```

```
9
 59 PAAGESAAPVPTAPAAGAPLMDFGNDFVPPAPRGPLPAAPPVAPERQPSWDPSPVSSTVP 118
 178
 61 PAAGLSAAAVP--PAAAAPLLDFSSDSVPPAPRGPLPAAPPAAPERQPSWERSPAA---P 115
 116 APSLPPAAAVLPSKLPEDDEPPARPPPPAGASPLAE------PAAPPSTPAAPKR 166
 225
 179 RGSSGSVVVDLLYWRDIKKTGVVFGASLFLLSLTVFSIVSVTAYIALALLSVTISFRIY 238
 285
 SLKFAVLMWVFTYVGALFNGLTLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAM 358
 SLKFAVLMWVFTYVGALFNGLTLLILALISLFSIPVIYERHQVQIDHYLGLANKSVKDAM 345
 8
 28
 1 MEDIDQSSLVSSSTDSPPRPPRFKYQFVTEPEDBEDEEEEEDDEBLEELEVLERK
 119 APSPLSAAAVSPSKLPEDDEPPARPPPPPASVSPQAEPVWTPPAPAAPPSTPAAPKR
 KGVIQAIQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRLFLVDDLVD
 RG-SGSSVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAY1ALALLSVTISFRIY
 MAGI protein; neuroendocrine-specific protein; neuropathy; human; spinal injury; neuronal degeneration; neuromuscular disorder; cancer; psychiatric disorder; developmental disorder; inflammatory disorder; stroke; cytostatic; cerebroprotective; neuroprotective; variant.
 Gaps
 Novel polypeptides related to neuroendocrine-specific proteins and polynucleotides useful for diagnosis of various diseases and for treatment of cancer and neurological disorders.
 17;
 DB 3; Length 373;
 Indels
 20;
 Pred. No. 1.4e-56;
11; Mismatches 20
 87.9%; Score 1603.3;
 AAY56969 standard; protein; 373 AA.
 Claim 2; Page 22; 35pp; English
 Human MAGI polypeptide variant.
 (SMIK) SMITHKLINE BEECHAM PLC.
 98GB-00016024.
99GB-00016898.
 99WO-GB002360.
 87.2%;
 346 AKIQAKIPGLKRKAD 360
 Prinjha RK;
 (first entry)
Query Match
Best Local Similarity 87.2⁷
***rhes 327; Conservative
 WPI; 2000-182693/16.
 N-PSDB; AAZ56888.
 WO200005364-A1.
 Michalovich D,
 sapiens.
 21-JUL-1999;
 22-JUL-1998;
 19-JUL-1999;
 25-APR-2000
 03-FEB-2000
 239
 359
 AAY56969;
 167
 226
 286
 299
 Ношон
 RESULT 15
 SX TY THE SY TO SEE THE SY TO SE THE SY TO SEE THE SY TO SE THE SY TO SE THE SY TO SE
```

They can be used for growth or differentiation of bone, cartilage, tendon, ligament, or nerve tissue, as well as for wound healing and tissue repair and replacement, and in the treatment of burns, incisions and ulcers, to induce cartilage and/or bone growth in circumstances where bone is not normally formed and thus have an application in healing bone

fractures and cartilage damage or defects, prophylactic use in fracture reduction and also in the improved fixation of artificial joints

```
The invention relates to human MAGI protein, which is similar to neuroendocrine-specific protein. The MAGI protein can be expressed by standard recombinant methodology. The MAGI polypeptides, polynucleotides and antibodies are useful for treating diseases, including neuropathies, spinal injury, neuronal degeneration, neuromuscular disorders, psychiatric disorders and developmental disorders, cancer, stroke and inflammatory disorders. The polynucleoitde is also useful for chromosome localization and for tissue expression studies. The present sequence represents the human MAGI protein variant
X888888888888XX
```

Sequence 373 AA;

PAAGLSAAAVP--PAAAAPLLDFSSDSVPPAPRGPLPAAPPAAPERQPSWERSPAA---P 115 APSLPPAAAVLPSKLPEDDEPPARPPPPAGASPLAE-----PAAPPSTPAAPKR 166 RG-SGSSVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIY 225 KGVIQAIQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRLFLVDDLVD 285 SLKFAVLMWVFTYVGALFNGLTLLILALISLFSIPVIYERHQVQIDHYLGLANKSVKDAM 345 9 MEDIDQSSLVSSSTDSPPRPPAFKYQFVTEPEDEEDEEBBEEBDEEDDLEELEVLERK 20; Indels 17; Gaps 87.9%; Score 1603.3; DB 3; Length 373; 87.2%; Pred. No. 1.4e-56; tive 11; Mismatches 20; Indels 17; AKIQAKIPGLKRKAD 360 359 AKIQAKIPGLKRKAE 373 Query Match Best Local Similarity 87.2% Matches 327; Conservative 61 59 116 119 167 179 226 239 286 299 346 ઠે 셤 ò qq ò ď à ď ઠે g ò a ઠે

Search completed: June 23, 2005, 10:52:00 Job time : 119.842 secs

a

```
GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
```

OM protein - protein search, using sw model

Run on:

June 23, 2005, 10:29:31; Search time 24.9653 Seconds (without alignments) 1387.446 Million cell updates/sec

US-09-830-972-2-FUSED

Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.1 Scoring table:

283416 segs, 96216763 residues Searched:

283416 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR 79:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

|           | Description    | neuroendocrine-spe | neuroendocrine-spe | tropomyosin-relate | hypothetical prote |        |        |        |        | hypothetical prote | cappuccino gene pr | leukocyte formin p | formin isoform IV | unconventional myo | Be     | hypothetical prote | probable Pto kinas | hypothetical prote | diaphanous protein | proline-rich prote | unknown protein (i | DNA topoisomerase | hypothetical prote | hypothetical prote | transcription regu | hypothetical prote |        | unconventional myo | tical p | FREAC-4 - human |
|-----------|----------------|--------------------|--------------------|--------------------|--------------------|--------|--------|--------|--------|--------------------|--------------------|--------------------|-------------------|--------------------|--------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|-------------------|--------------------|--------------------|--------------------|--------------------|--------|--------------------|---------|-----------------|
| SUMMARIES | ID             | A46583             | I60904             | A60021             | T26216             | T26215 | T26213 | A35466 | T31421 | T38236             | T13286             | JC8033             | S24407            | A59266             | S11515 | T26998             | F86387             | C96623             | T31065             | S71461             | G86441             | JC6552            | E96636             | T19536             | T39371             | A71416             | EDBEIF | A59295             | 57      | G02738          |
|           | DB             | 7                  | ~                  | ~                  | 0                  | ~      | ~      | ~      | ~      | ~                  | ~                  | ~                  | ~                 | ~                  | ~      | ~                  | N                  | ~                  | ~                  | ~                  | ~                  | ~                 | ~                  | ~                  | 7                  | 7                  | -      | ~                  | N       | 7               |
|           | Length         | 776                |                    |                    |                    |        | 222    |        |        |                    |                    |                    |                   | 3530               |        | 716                | 760                | 929                | 1255               | 2157               | 1201               | 1015              | 907                | 1657               | 1522               | 645                | 1460   | 3511               | 710     | 465             |
| di        | Query<br>Match | 45.3               | 37.5               | 36.7               | 24.0               | 23.4   | 18.5   | 14.9   | 14.6   | 14.6               | 14.2               | 14.1               | 14.1              | 14.1               | 14.0   | 14.0               | 13.9               | 13.9               | 13.9               | 13.8               | 13.8               | 13.8              | 13.7               | 13.5               | 13.5               | 13.5               | 13.5   | 13.5               | 13.4    | 13.4            |
|           | Score          | œ                  | 683                | 699                | 437.7              | 427.4  | 337.5  | 272.1  | 266.9  | 265.5              | 258.5              | 257.8              | 257.5             | 256.4              | 254.9  | 254.7              | 253.8              | 253.2              | 253.2              | 252.2              | 251.9              | 250.9             | 250.2              | 246.4              | 246                | 245.8              | 245.4  | 245.2              | 245.1   | 244.7           |
|           | Result<br>No.  |                    | 7                  | ٣                  | 4                  | 2      | 9      | 7      | 80     | <b>о</b>           | 10                 | 11                 | 12                | 13                 | 14     | 15                 | 16                 | 17                 | 18                 | 19                 | 20                 | 21                | 22                 | 23                 | 24                 | 25                 | 26     | 27                 | 28      | 29              |

| 30 244.3 13.4 1064 2 T19963<br>31 242.7 13.3 1573 2 700344<br>32 242.1 13.3 1573 2 768375<br>33 241.9 13.3 1213 2 A5198<br>35 241.7 13.3 3938 2 A5198<br>36 240.9 13.2 980 2 G75523<br>37 240.6 13.2 1634 2 T26517<br>38 240.6 13.2 1634 2 T26517<br>39 238.9 13.1 1446 1 A4534<br>40 238.5 13.1 1047 2 A55617<br>41 238.5 13.1 1047 2 A55617<br>42 238.4 13.1 3149 1 QQBE8<br>43 237.5 13.0 980 2 S54986 | formin related pro | hypothetical prote | hypothetical prote | serine/proline-ric | Bassoon protein - | immediate-early pr | probable cell divi | hypothetical prote | immediate-early pr | hypothetical prote | masquerade precurs | probable cytoskele | elastic titin - hu | BPLF1 protein - hu | progesterone recep | regulatory protein |
|-----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|--------------------|--------------------|--------------------|--------------------|-------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|
| 4                                                                                                                                                                                                                                                                                                                                                                                                         | T13963             | T00344             | 848375             | A58198             | T42761            | EDBE11             | G75523             | T26517             | A45344             | T04455             | A55617             | T37781             | I38346             | QQBE8              | QRHUP              | S54986             |
| 4                                                                                                                                                                                                                                                                                                                                                                                                         | ~                  | ~                  | N                  | N                  | ~                 | н                  | ~                  | ~                  | -                  | N                  | N                  | ~                  | N                  | ч                  | н                  | N                  |
|                                                                                                                                                                                                                                                                                                                                                                                                           | 1064               | 1533               | 1375               | 1213               | 3938              | 775                | 980                | 1634               | 1446               | 731                | 1047               | 1420               | 7962               | 3149               | 933                | 980                |
| 330<br>331<br>332<br>333<br>333<br>334<br>335<br>336<br>336<br>336<br>336<br>336<br>336<br>336<br>336<br>336                                                                                                                                                                                                                                                                                              | 13.4               | 13.3               | 13.3               | 13.3               | 13.3              | 13.2               | 13.2               | 13.2               | 13.2               | 13.1               | 13.1               | 13.1               | 13.1               | 13.1               | 13.0               | 13.0               |
| 30<br>311<br>32<br>33<br>34<br>34<br>44<br>44<br>44<br>44<br>44<br>44<br>44<br>44                                                                                                                                                                                                                                                                                                                         | 244.3              | 242.7              | 242.1              | 241.9              | 241.7             | 241.1              | 240.9              | 240.6              | 240.5              | 238.9              | 238.5              | 238.5              | 238.4              | 238                | 237.6              | 237.5              |
|                                                                                                                                                                                                                                                                                                                                                                                                           | 30                 | 31                 | 32                 | 33                 | 34                | 35                 | 36                 | 37                 | 38                 | 39                 | 40                 | 41                 | 42                 | 43                 | 44                 | 45                 |

## ALIGNMENTS

|             | RESULT 1                                                                |                                                                                                                                                                |
|-------------|-------------------------------------------------------------------------|----------------------------------------------------------------------------------------------------------------------------------------------------------------|
|             | neuroendocrin<br>N;Contains: 1                                          | Agesos<br>neuroendocrine-specific protein, splice form A - human<br>N;Contains: neuroendocrine-specific protein, splice form B<br>C:Species Homo samiens (man) |
|             | C;Date: 24-M:<br>C:Accession:                                           | C.Date: 24. May-1996 #sequence_revision 24-May-1996 #text_change 09-Jul-2004<br>C.Dates Afs 1860903                                                            |
|             | R;Roebroek, J                                                           | R.Roebroek, A.J.; van de Velde, H.J.; Van Bokhoven, A.; Broers, J.L.; Ramaekers, F.C.; Va<br>J. Biol. Chem. 268, 13439-13447, 1993                             |
|             | A, Title: Clor<br>A, Reference                                          | A;Title: Cloning and expression of alternative transcripts of a novel neuroendocrine-spec<br>A;Reference number: A46583; MUID:93293865; PMID:7685762           |
|             | A;Accession: A46583<br>A;Status: preliminary<br>A;Molecule type: mRNA   | A;Accession: Afobsy<br>A;Status: preliminary; translated from GB/EMBL/DDBJ<br>A;Molecule type: mRNA                                                            |
|             | A; Residues: 1-776 < ROE1> A; Cross-references: UNIP                    | A;Residues: 1-776 <roe1><br/>A;Cross_references: UNIPROT:Q16799; GB:L10333; NID:g307306; PIDN:AAA59950.1; PID:g307307</roe1>                                   |
|             | A;Accession: 160903<br>A;Status: prelimina                              | A;Accession: iouyus<br>Azetus: preliminary; translated from GB/EMBL/DDBJ<br>A:McToculo trace, muna                                                             |
|             | A;Residues:                                                             | A.Residues: 421-712. "Maria<br>A.Residues: 421-712 (ROE2><br>A.Cross-references: CR-1,10334. NID.G20730R. DIDN.ABAE9951 1. DID.G307309                         |
|             | C, Genetics:                                                            | 11.11.12.12.13.13.12.12.13.13.13.13.13.13.13.13.13.13.13.13.13.                                                                                                |
|             | A;Gene: GDB:KTN1; NSP<br>A;Cross-references: G<br>A;Map position: 14Q21 | A;Gene: GDB:KTVI, NB:203968; OMIM:600865<br>A;Cross-references: GDB:203968; OMIM:600865<br>A;Map position: 14q21-14q22                                         |
|             | Query Match<br>Best Local<br>Matches 19                                 | Query Match Best Local Similarity 27.7%; Pred. No. 6.7e-20; Matches 195; Conservative 52; Mismatches 91; Indels 367; Gaps 17;                                  |
|             | ογ 10                                                                   | 10 VSSSTDS 19                                                                                                                                                  |
|             | Db 85                                                                   | :  <br>. VSSAMDHTFSTTSKDGEGSCYTSLISDICYPPQEDSTYFTGILQKENGHVTISESPEELG 144                                                                                      |
|             |                                                                         |                                                                                                                                                                |
|             | Db 145                                                                  | 145 TPGPSLPDVPGIESRGLFSSDSGIEMTPAESTEVNKILADPLDQMKAEAYKYIDITRPEE 204                                                                                           |
|             | Qy 35                                                                   | EEDEEBEBEBEBEBEA508D50                                                                                                                                         |
|             | Db 205                                                                  | 205 VKHQEQHHPELEDKOLDFKNKDTDISIKPEGVREPDKPAPVEGKIIKDHLLEESTFAPYI 264                                                                                           |
|             | 0y 51                                                                   |                                                                                                                                                                |
| <del></del> | Db 26                                                                   | 265 DDLSEEQRRAPQITTPVKITLTEIEPSVETTTQEKTPEKQDICLKPSPDTVPTVTVSEPÈ 324                                                                                           |
|             | Qy 56                                                                   | VLERKPAAGLS 66                                                                                                                                                 |
|             | Db 325                                                                  | DDSPGSITPPSSGTEPSAAESQGKGSISEDELITAIKEAKGLSYETAENPRPVGQLADRP 384                                                                                               |
|             | Qy 67                                                                   | .    .    .   .   .                                                                                                                                            |
| •           |                                                                         |                                                                                                                                                                |

| DD   385 EVKARSGPPTIPSP-LDHEASSAESGDSEIELVSEDPMAEDALPSGYVSFGHVGGPPPS 443   0                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   | C;Accession: A60021  R;Wieczork, D.F.; Hughes, S.R.  Brain Res. Mol. Brain Res. 10, 33-41, 1991  Brain Res. Mol. Brain Res. 10, 33-41, 1991  A;Tille: Developmentally regulated cDNA expressed exclusively in neural tissue.  A;Reference number: A60021  A;Reference number: A60021  A;Residues: 1-267 cWIB-  A;Ccossion: A60021  A;Residues: 1-267 cWIB-  A;Ccossion: A60021  A;Residues: 1-267 cWIB-  A;Ccossion: A60021  A;Ccossion: A60021  A;Residues: 1-267 cWIB-  A;Ccossion: A60021  A;Residues: 1-267 cWIB-  A;Ccossion: A60021  A;Residues: 1-267 cWIB-  A;Residues: 1-267 cWIB-  A;Ccossion: A60021  A;Residues: 1-267 cWIB-  ;Residues: 1-267 cWIB- A;Residues: 1-267 cWIB- A;Residues: 1-267 cWIB- A;Residues: 1-267 cWIB- A;Residues: 1-267 cWIB- A;Residues: 1-267 cWIB- A;Residues: 1-267 cWIB- A;Residues: 1-267 cWIB- A;Residues: 1-267 cWIB- A;Residues: 1-267 cWIB- A;Residues: 1-267 cWIB- A;Residues: 1-267 cWIB- A;Residues: 1-267 cWIB- A;Residues: 1-267 cWIB- A;Residues: 1-267 cWIB- A;Residues: 1-267 cWIB- A;Residue: 1-267 cWIB- A;Re |
|--------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|--------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| **Specific protein C - human O sapiens (man) -1996 #sequence_revision 24-May-1996 #text_change 60904 3. van de Velde, H.J.; Van Bokhoven, A.; Broers, 268, 13439-13447, 1993 ng and expression of alternative transcripts of a mber: A46583; MUID:93293865; PMID:7685762 ininary; translated from GB/EMBL/DDBJ e: mRNA 208 *RES> NN; NSP NCCes: UNIPROT:Q16799; GB:L10335; NID:g307310; PID) NN; NSP ncces: GDB:203968; OMIM:600865                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            | Qy 351 KIPGLK 356          :                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   |
| Query Match  37.5%; Score 683; DB 2; Length 208;  Best Local Similarity 67.4%; Pred. No. 1.86-16;  Matches 128; Conservative 31; Mismatches 31; Indels 0; Gaps 0;  Qy 171 SSVVDLLYWEDIKKTGVVFGASLFLLSTVFSIVSVTAXIALLSVTISFRIYKGVIQ 230  Db 19 SQAIDLLYWRDIKQTGIVFGSFLLLFSLTQFSVVSVVAYLALAALSATISFRIYKSVLQ 78  ON 231 AIOKENECHPPRANIEGEVALGEFLYORVSNOALCHVNSTIKFIDDLEINDNINGIEFR 200                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           | C;Genetics: A;Gene: CESP:WGA7.3c A;Gene: CESP:WGA7.3c A;Map position: 5 A;Introns: 1827/1; 1866/3; 1963/3; 1990/3; 2262/1; 2289/1; 2339/2; 2463/2 A;Introns: 1827/1; 1866/3; 1963/3; 1990/3; 2262/1; 2289/1; 2339/2; 2463/2 A;Introns: 1827/1; 1866/3; 1963/3; 1990/3; 2262/1; 2289/1; 2389/2; 2463/2 Guery Match Best Local Similarity 14.8%; Pred. No. 1.5e-05; Matches 135; Conservative 77; Mismatches 138; Indels 563; Gaps 21;                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           |
| 231 AUGNETITY CALLES VALUES EL VOIT STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STA | OY 1 MEDIDOSSLVSSST                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            |
| RESULT 3<br>A60021<br>tropomyosin-related protein, neuronal - rat<br>C;Species: Rattus norvegicus (Norway rat)<br>C;Date: 03-Mar-1993 #sequence_revision 03-Mar-1993 #text_change 05-Nov-1999                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  | Qy         45                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  |

| 15   16   16   16   16   16   16   16                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        | 1806 SECLDSIGDLSERTIQRFNTSIDDPSIRRDSF8SISSFGDRQKFRTALENIRQDLLPFQS 1865                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         | 셤          | : :                                                              |
|------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|--------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|------------|------------------------------------------------------------------|
| 1.516 EGAPATHORN PROPERTY CONTRIBUTION   1.516 EGAPATHORN PROPERTY CONTRIBUTION   1.516 EGAPATHORN PROPERTY CONTRIBUTION   1.516 EGAPATHORN PROPERTY CONTRIBUTION   1.516 EGAPATHORN PROPERTY CONTRIBUTION   1.516 EGAPATHORN PROPERTY CONTRIBUTION   1.516 EGAPATHORN PROPERTY CONTRIBUTION   1.516 EGAPATHORN PROPERTY CONTRIBUTION   1.516 EGAPATHORN PROPERTY CONTRIBUTION   1.516 EGAPATHORN PROPERTY CONTRIBUTION   1.516 EGAPATHORN PROPERTY CONTRIBUTION   1.516 EGAPATHORN PROPERTY CONTRIBUTION   1.516 EGAPATHORN PROPERTY CONTRIBUTION   1.516 EGAPATHORN PROPERTY CONTRIBUTION   1.516 EGAPATHORN PROPERTY CONTRIBUTION   1.516 EGAPATHORN PROPERTY CONTRIBUTION   1.516 EGAPATHORN PROPERTY CONTRIBUTION   1.516 EGAPATHORN PROPERTY CONTRIBUTION   1.516 EGAPATHORN PROPERTY CONTRIBUTION   1.516 EGAPATHORN PROPERTY CONTRIBUTION   1.516 EGAPATHORN PROPERTY CONTRIBUTION   1.516 EGAPATHORN PROPERTY CONTRIBUTION   1.516 EGAPATHORN PROPERTY CONTRIBUTION   1.516 EGAPATHORN PROPERTY CONTRIBUTION   1.516 EGAPATHORN PROPERTY CONTRIBUTION   1.516 EGAPATHORN PROPERTY CONTRIBUTION   1.516 EGAPATHORN PROPERTY CONTRIBUTION   1.516 EGAPATHORN PROPERTY CONTRIBUTION   1.516 EGAPATHORN PROPERTY CONTRIBUTION   1.516 EGAPATHORN PROPERTY CONTRIBUTION   1.516 EGAPATHORN PROPERTY CONTRIBUTION   1.516 EGAPATHORN PROPERTY CONTRIBUTION   1.516 EGAPATHORN PROPERTY CONTRIBUTION   1.516 EGAPATHORN PROPERTY CONTRIBUTION   1.516 EGAPATHORN PROPERTY CONTRIBUTION   1.516 EGAPATHORN PROPERTY CONTRIBUTION   1.516 EGAPATHORN PROPERTY CONTRIBUTION   1.516 EGAPATHORN PROPERTY CONTRIBUTION   1.516 EGAPATHORN PROPERTY CONTRIBUTION   1.516 EGAPATHORN PROPERTY CONTRIBUTION   1.516 EGAPATHORN PROPERTY CONTRIBUTION   1.516 EGAPATHORN PROPERTY CONTRIBUTION   1.516 EGAPATHORN PROPERTY CONTRIBUTION   1.516 EGAPATHORN PROPERTY CONTRIBUTION   1.516 EGAPATHORN PROPERTY CONTRIBUTION   1.516 EGAPATHORN PROPERTY CONTRIBUTION   1.516 EGAPATHORN PROPERTY CONTRIBUTION   1.516 EGAPATHORN PROPERTY CONTRIBUTION   1.516 EGAPATHORN PROPERTY CONTRIBUTION   1.516 EGAPATHORN PROPERTY CONTRIBUT | ERKPAA                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         | ò          | DSPPRPPAFKYQFVTEPEDE3                                            |
|                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              | 1866 SVSQYLRSSPNPSQQLLVTNLSMDSPSDLSPNAPPVGFENTAQFLEKLQQEDRPSAEGSI 192                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          | 셤          |                                                                  |
| 146   111170QPPSETTEMPLANE   126   126   126   126   126   126   126   126   126   126   126   126   126   126   126   126   126   126   126   126   126   126   126   126   126   126   126   126   126   126   126   126   126   126   126   126   126   126   126   126   126   126   126   126   126   126   126   126   126   126   126   126   126   126   126   126   126   126   126   126   126   126   126   126   126   126   126   126   126   126   126   126   126   126   126   126   126   126   126   126   126   126   126   126   126   126   126   126   126   126   126   126   126   126   126   126   126   126   126   126   126   126   126   126   126   126   126   126   126   126   126   126   126   126   126   126   126   126   126   126   126   126   126   126   126   126   126   126   126   126   126   126   126   126   126   126   126   126   126   126   126   126   126   126   126   126   126   126   126   126   126   126   126   126   126   126   126   126   126   126   126   126   126   126   126   126   126   126   126   126   126   126   126   126   126   126   126   126   126   126   126   126   126   126   126   126   126   126   126   126   126   126   126   126   126   126   126   126   126   126   126   126   126   126   126   126   126   126   126   126   126   126   126   126   126   126   126   126   126   126   126   126   126   126   126   126   126   126   126   126   126   126   126   126   126   126   126   126   126   126   126   126   126   126   126   126   126   126   126   126   126   126   126   126   126   126   126   126   126   126   126   126   126   126   126   126   126   126   126   126   126   126   126   126   126   126   126   126   126   126   126   126   126   126   126   126   126   126   126   126   126   126   126   126   126   126   126   126   126   126   126   126   126   126   126   126   126   126   126   126   126   126   126   126   126   126   126   126   126   126   126   126   126   126   126   126   126   126   126   126   126   126   126   126   126   126   | 64GLSAAAVPP                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    | ò          |                                                                  |
| 100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100  | 1926 DSSGFEKVDHEGLDEFAAPPVHDPMQKSVFGSLGSDDMKPGSQDDGFVFIERNEANEATL                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              | qq         |                                                                  |
| 11-46   SEPONDATE PARTICULAR PARTICULAR PARTICULAR PARTICULAR PARTICULAR PARTICULAR PARTICULAR PARTICULAR PARTICULAR PARTICULAR PARTICULAR PARTICULAR PARTICULAR PARTICULAR PARTICULAR PARTICULAR PARTICULAR PARTICULAR PARTICULAR PARTICULAR PARTICULAR PARTICULAR PARTICULAR PARTICULAR PARTICULAR PARTICULAR PARTICULAR PARTICULAR PARTICULAR PARTICULAR PARTICULAR PARTICULAR PARTICULAR PARTICULAR PARTICULAR PARTICULAR PARTICULAR PARTICULAR PARTICULAR PARTICULAR PARTICULAR PARTICULAR PARTICULAR PARTICULAR PARTICULAR PARTICULAR PARTICULAR PARTICULAR PARTICULAR PARTICULAR PARTICULAR PARTICULAR PARTICULAR PARTICULAR PARTICULAR PARTICULAR PARTICULAR PARTICULAR PARTICULAR PARTICULAR PARTICULAR PARTICULAR PARTICULAR PARTICULAR PARTICULAR PARTICULAR PARTICULAR PARTICULAR PARTICULAR PARTICULAR PARTICULAR PARTICULAR PARTICULAR PARTICULAR PARTICULAR PARTICULAR PARTICULAR PARTICULAR PARTICULAR PARTICULAR PARTICULAR PARTICULAR PARTICULAR PARTICULAR PARTICULAR PARTICULAR PARTICULAR PARTICULAR PARTICULAR PARTICULAR PARTICULAR PARTICULAR PARTICULAR PARTICULAR PARTICULAR PARTICULAR PARTICULAR PARTICULAR PARTICULAR PARTICULAR PARTICULAR PARTICULAR PARTICULAR PARTICULAR PARTICULAR PARTICULAR PARTICULAR PARTICULAR PARTICULAR PARTICULAR PARTICULAR PARTICULAR PARTICULAR PARTICULAR PARTICULAR PARTICULAR PARTICULAR PARTICULAR PARTICULAR PARTICULAR PARTICULAR PARTICULAR PARTICULAR PARTICULAR PARTICULAR PARTICULAR PARTICULAR PARTICULAR PARTICULAR PARTICULAR PARTICULAR PARTICULAR PARTICULAR PARTICULAR PARTICULAR PARTICULAR PARTICULAR PARTICULAR PARTICULAR PARTICULAR PARTICULAR PARTICULAR PARTICULAR PARTICULAR PARTICULAR PARTICULAR PARTICULAR PARTICULAR PARTICULAR PARTICULAR PARTICULAR PARTICULAR PARTICULAR PARTICULAR PARTICULAR PARTICULAR PARTICULAR PARTICULAR PARTICULAR PARTICULAR PARTICULAR PARTICULAR PARTICULAR PARTICULAR PARTICULAR PARTICULAR PARTICULAR PARTICULAR PARTICULAR PARTICULAR PARTICULAR PARTICULAR PARTICULAR PARTICULAR PARTICULAR PARTICULAR PARTICULAR PARTICULAR PARTICULAR PARTICULAR PARTICULAR PARTICULAR PARTICULAR PARTICULAR PA | AAAADLL-                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       | ò          | BEDDEDLEBLEVI                                                    |
| Procession   Procession   Procession   Procession   Procession   Procession   Procession   Procession   Procession   Procession   Procession   Procession   Procession   Procession   Procession   Procession   Procession   Procession   Procession   Procession   Procession   Procession   Procession   Procession   Procession   Procession   Procession   Procession   Procession   Procession   Procession   Procession   Procession   Procession   Procession   Procession   Procession   Procession   Procession   Procession   Procession   Procession   Procession   Procession   Procession   Procession   Procession   Procession   Procession   Procession   Procession   Procession   Procession   Procession   Procession   Procession   Procession   Procession   Procession   Procession   Procession   Procession   Procession   Procession   Procession   Procession   Procession   Procession   Procession   Procession   Procession   Procession   Procession   Procession   Procession   Procession   Procession   Procession   Procession   Procession   Procession   Procession   Procession   Procession   Procession   Procession   Procession   Procession   Procession   Procession   Procession   Procession   Procession   Procession   Procession   Procession   Procession   Procession   Procession   Procession   Procession   Procession   Procession   Procession   Procession   Procession   Procession   Procession   Procession   Procession   Procession   Procession   Procession   Procession   Procession   Procession   Procession   Procession   Procession   Procession   Procession   Procession   Procession   Procession   Procession   Procession   Procession   Procession   Procession   Procession   Procession   Procession   Procession   Procession   Procession   Procession   Procession   Procession   Procession   Procession   Procession   Procession   Procession   Procession   Procession   Procession   Procession   Procession   Procession   Procession   Procession   Procession   Procession   Procession   Procession   Procession   Procession   Pro | 1986 KKNQKMSSHHNDVIEKNYFNDNAPTAALLESPIAEEARKIVQDAVESASEYKKQAVDSGD                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              | q          |                                                                  |
| 100   SECTION CONTRICTOR CONTRICTOR CONTRICTOR CONTRICTOR CONTRICTOR CONTRICTOR CONTRICTOR CONTRICTOR CONTRICTOR CONTRICTOR CONTRICTOR CONTRICTOR CONTRICTOR CONTRICTOR CONTRICTOR CONTRICTOR CONTRICTOR CONTRICTOR CONTRICTOR CONTRICTOR CONTRICTOR CONTRICTOR CONTRICTOR CONTRICTOR CONTRICTOR CONTRICTOR CONTRICTOR CONTRICTOR CONTRICTOR CONTRICTOR CONTRICTOR CONTRICTOR CONTRICTOR CONTRICTOR CONTRICTOR CONTRICTOR CONTRICTOR CONTRICTOR CONTRICTOR CONTRICTOR CONTRICTOR CONTRICTOR CONTRICTOR CONTRICTOR CONTRICTOR CONTRICTOR CONTRICTOR CONTRICTOR CONTRICTOR CONTRICTOR CONTRICTOR CONTRICTOR CONTRICTOR CONTRICTOR CONTRICTOR CONTRICTOR CONTRICTOR CONTRICTOR CONTRICTOR CONTRICTOR CONTRICTOR CONTRICTOR CONTRICTOR CONTRICTOR CONTRICTOR CONTRICTOR CONTRICTOR CONTRICTOR CONTRICTOR CONTRICTOR CONTRICTOR CONTRICTOR CONTRICTOR CONTRICTOR CONTRICTOR CONTRICTOR CONTRICTOR CONTRICTOR CONTRICTOR CONTRICTOR CONTRICTOR CONTRICTOR CONTRICTOR CONTRICTOR CONTRICTOR CONTRICTOR CONTRICTOR CONTRICTOR CONTRICTOR CONTRICTOR CONTRICTOR CONTRICTOR CONTRICTOR CONTRICTOR CONTRICTOR CONTRICTOR CONTRICTOR CONTRICTOR CONTRICTOR CONTRICTOR CONTRICTOR CONTRICTOR CONTRICTOR CONTRICTOR CONTRICTOR CONTRICTOR CONTRICTOR CONTRICTOR CONTRICTOR CONTRICTOR CONTRICTOR CONTRICTOR CONTRICTOR CONTRICTOR CONTRICTOR CONTRICTOR CONTRICTOR CONTRICTOR CONTRICTOR CONTRICTOR CONTRICTOR CONTRICTOR CONTRICTOR CONTRICTOR CONTRICTOR CONTRICTOR CONTRICTOR CONTRICTOR CONTRICTOR CONTRICTOR CONTRICTOR CONTRICTOR CONTRICTOR CONTRICTOR CONTRICTOR CONTRICTOR CONTRICTOR CONTRICTOR CONTRICTOR CONTRICTOR CONTRICTOR CONTRICTOR CONTRICTOR CONTRICTOR CONTRICTOR CONTRICTOR CONTRICTOR CONTRICTOR CONTRICTOR CONTRICTOR CONTRICTOR CONTRICTOR CONTRICTOR CONTRICTOR CONTRICTOR CONTRICTOR CONTRICTOR CONTRICTOR CONTRICTOR CONTRICTOR CONTRICTOR CONTRICTOR CONTRICTOR CONTRICTOR CONTRICTOR CONTRICTOR CONTRICTOR CONTRICTOR CONTRICTOR CONTRICTOR CONTRICTOR CONTRICTOR CONTRICTOR CONTRICTOR CONTRICTOR CONTRICTOR CONTRICTOR CONTRICTOR CONTRICTOR CONTRICTOR CONTRICTOR CONTRICTOR CONTRICTOR CONTRICTOR CONTRI | DESSDSVPPAPRGPL                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                | ò          |                                                                  |
| Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part    | EIGRELLDNVEQKIEQVKEPIVDSLHKAYDGVGDFVHETVPNAVDDFVREAEKQLPESPV                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   | 셤          | SECLDSIGDLSERTIQRFNTSIDDPSIRRDSFSSISSFGDRQKFRTAIENIRQDLLPFQS 186 |
| Particle   Particle   Particle   Particle   Particle   Particle   Particle   Particle   Particle   Particle   Particle   Particle   Particle   Particle   Particle   Particle   Particle   Particle   Particle   Particle   Particle   Particle   Particle   Particle   Particle   Particle   Particle   Particle   Particle   Particle   Particle   Particle   Particle   Particle   Particle   Particle   Particle   Particle   Particle   Particle   Particle   Particle   Particle   Particle   Particle   Particle   Particle   Particle   Particle   Particle   Particle   Particle   Particle   Particle   Particle   Particle   Particle   Particle   Particle   Particle   Particle   Particle   Particle   Particle   Particle   Particle   Particle   Particle   Particle   Particle   Particle   Particle   Particle   Particle   Particle   Particle   Particle   Particle   Particle   Particle   Particle   Particle   Particle   Particle   Particle   Particle   Particle   Particle   Particle   Particle   Particle   Particle   Particle   Particle   Particle   Particle   Particle   Particle   Particle   Particle   Particle   Particle   Particle   Particle   Particle   Particle   Particle   Particle   Particle   Particle   Particle   Particle   Particle   Particle   Particle   Particle   Particle   Particle   Particle   Particle   Particle   Particle   Particle   Particle   Particle   Particle   Particle   Particle   Particle   Particle   Particle   Particle   Particle   Particle   Particle   Particle   Particle   Particle   Particle   Particle   Particle   Particle   Particle   Particle   Particle   Particle   Particle   Particle   Particle   Particle   Particle   Particle   Particle   Particle   Particle   Particle   Particle   Particle   Particle   Particle   Particle   Particle   Particle   Particle   Particle   Particle   Particle   Particle   Particle   Particle   Particle   Particle   Particle   Particle   Particle   Particle   Particle   Particle   Particle   Particle   Particle   Particle   Particle   Particle   Particle   Particle  | PBRQ                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           | ò          |                                                                  |
| STATE                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        | PEKIETPEPLVDIHDTVDKVHDBVDNFLRREPTPPFETDDVAPLSDDKPQFGNQTPEEDE                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   | qq         | SVSQYLRSSPNPSQQLLVTNLSMDSPSDLSPNAPPVGFENTAQFLEKLQQEDRPSAEGSI 192 |
| Pack   Pack   Pack   Pack   Pack   Pack   Pack   Pack   Pack   Pack   Pack   Pack   Pack   Pack   Pack   Pack   Pack   Pack   Pack   Pack   Pack   Pack   Pack   Pack   Pack   Pack   Pack   Pack   Pack   Pack   Pack   Pack   Pack   Pack   Pack   Pack   Pack   Pack   Pack   Pack   Pack   Pack   Pack   Pack   Pack   Pack   Pack   Pack   Pack   Pack   Pack   Pack   Pack   Pack   Pack   Pack   Pack   Pack   Pack   Pack   Pack   Pack   Pack   Pack   Pack   Pack   Pack   Pack   Pack   Pack   Pack   Pack   Pack   Pack   Pack   Pack   Pack   Pack   Pack   Pack   Pack   Pack   Pack   Pack   Pack   Pack   Pack   Pack   Pack   Pack   Pack   Pack   Pack   Pack   Pack   Pack   Pack   Pack   Pack   Pack   Pack   Pack   Pack   Pack   Pack   Pack   Pack   Pack   Pack   Pack   Pack   Pack   Pack   Pack   Pack   Pack   Pack   Pack   Pack   Pack   Pack   Pack   Pack   Pack   Pack   Pack   Pack   Pack   Pack   Pack   Pack   Pack   Pack   Pack   Pack   Pack   Pack   Pack   Pack   Pack   Pack   Pack   Pack   Pack   Pack   Pack   Pack   Pack   Pack   Pack   Pack   Pack   Pack   Pack   Pack   Pack   Pack   Pack   Pack   Pack   Pack   Pack   Pack   Pack   Pack   Pack   Pack   Pack   Pack   Pack   Pack   Pack   Pack   Pack   Pack   Pack   Pack   Pack   Pack   Pack   Pack   Pack   Pack   Pack   Pack   Pack   Pack   Pack   Pack   Pack   Pack   Pack   Pack   Pack   Pack   Pack   Pack   Pack   Pack   Pack   Pack   Pack   Pack   Pack   Pack   Pack   Pack   Pack   Pack   Pack   Pack   Pack   Pack   Pack   Pack   Pack   Pack   Pack   Pack   Pack   Pack   Pack   Pack   Pack   Pack   Pack   Pack   Pack   Pack   Pack   Pack   Pack   Pack   Pack   Pack   Pack   Pack   Pack   Pack   Pack   Pack   Pack   Pack   Pack   Pack   Pack   Pack   Pack   Pack   Pack   Pack   Pack   Pack   Pack   Pack   Pack   Pack   Pack   Pack   Pack   Pack   Pack   Pack   Pack   Pack   Pack   Pack   Pack   Pack   Pack   Pack   Pack   Pack   Pack   Pack   Pack   Pack   Pack   Pack   Pack   Pack   Pack   Pack   Pack   Pack   Pack   Pack   Pack   Pack   Pack   Pack   Pack    | PSWERSPAAPAPSLPPAAAVLPSKLPEDD                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  | ð í        |                                                                  |
|                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              | TTFDKKGFUTTPEEVEKAAAAQNNDLDDFDPLVISNIGAAFGAAVGAAAAVESLIEEE                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     | <u>a</u> 8 | DSSGFEKVDHEGLDEFAAPPVHDPMQKSVFGSLGSDDMKFGSQDDGFVFIEKNEANEAIL 198 |
| SEVUDLIAMEDIKKTOVPEGALFELLIGITVPSIVATATIALALISTISPR 223   09   2046 EIGRELLONVEGALFELLIGITVPSIVATATIALALISTISPR 223   09   2046 EIGRELLONVEGALFELLIGITVPSIVATATIALALISTISPR 223   09   2046 EIGRELLONVEGALFELLIGITVPSIVATATIALALISTICALISTICALISTICALISTICALISTICALISTICALISTICALISTICALISTICALISTICALISTICALISTICALISTICALISTICALISTICALISTICALISTICALISTICALISTICALISTICALISTICALISTICALISTICALISTICALISTICALISTICALISTICALISTICALISTICALISTICALISTICALISTICALISTICALISTICALISTICALISTICALISTICALISTICALISTICALISTICALISTICALISTICALISTICALISTICALISTICALISTICALISTICALISTICALISTICALISTICALISTICALISTICALISTICALISTICALISTICALISTICALISTICALISTICALISTICALISTICALISTICALISTICALISTICALISTICALISTICALISTICALISTICALISTICALISTICALISTICALISTICALISTICALISTICALISTICALISTICALISTICALISTICALISTICALISTICALISTICALISTICALISTICALISTICALISTICALISTICALISTICALISTICALISTICALISTICALISTICALISTICALISTICALISTICALISTICALISTICALISTICALISTICALISTICALISTICALISTICALISTICALISTICALISTICALISTICALISTICALISTICALISTICALISTICALISTICALISTICALISTICALISTICALISTICALISTICALISTICALISTICALISTICALISTICALISTICALISTICALISTICALISTICALISTICALISTICALISTICALISTICALISTICALISTICALISTICALISTICALISTICALISTICALISTICALISTICALISTICALISTICALISTICALISTICALISTICALISTICALISTICALISTICALISTICALISTICALISTICALISTICALISTICALISTICALISTICALISTICALISTICALISTICALISTICALISTICALISTICALISTICALISTICALISTICALISTICALISTICALISTICALISTICALISTICALISTICALISTICALISTICALISTICALISTICALISTICALISTICALISTICALISTICALISTICALISTICALISTICALISTICALISTICALISTICALISTICALISTICALISTICALISTICALISTICALISTICALISTICALISTICALISTICALISTICALISTICALISTICALISTICALISTICALISTICALISTICALISTICALISTICALISTICALISTICALISTICALISTICALISTICALISTICALISTICALISTICALISTICALISTICALISTICALISTICALISTICALISTICALISTICALISTICALISTICALISTICALISTICALISTICALISTICALISTICALISTICALISTICALISTICALISTICALISTICALISTICALISTICALISTICALISTICALISTICALISTICALISTICALISTICALISTICALISTICALISTICALISTICALISTICALISTICALISTICALISTICALISTICALISTICALISTICALISTICALISTICALISTICALISTICALISTICALISTICALISTICALISTICALISTICALISTICALISTICALISTICALISTICALISTICALISTICALISTICALISTICALISTICAL |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                | è 6        | KKNOKWSCHHNDVIEKNY PNDNAPTAILESPIAERERIJODAVESASEYKKOAVDSGD      |
|                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              | SQUVDI I WWDDI KKTKKKYKEASI, FI I I.SI TURRI VENTANA VI AI AI I.SI TURKI SEB                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   | ìè         | Iduad                                                            |
| 11   1   1   1   1   1   1   1   1                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                | <b>3</b> 8 | BIGRELLDNVEQKIEQVKEPIVDSLHKAYDGVGDFVHETVPNAVDDFVREAEKQLPESPV     |
| Decinosity   Decinosity   Decinosity   Decinosity   Decinosity   Decinosity   Decinosity   Decinosity   Decinosity   Decinosity   Decinosity   Decinosity   Decinosity   Decinosity   Decinosity   Decinosity   Decinosity   Decinosity   Decinosity   Decinosity   Decinosity   Decinosity   Decinosity   Decinosity   Decinosity   Decinosity   Decinosity   Decinosity   Decinosity   Decinosity   Decinosity   Decinosity   Decinosity   Decinosity   Decinosity   Decinosity   Decinosity   Decinosity   Decinosity   Decinosity   Decinosity   Decinosity   Decinosity   Decinosity   Decinosity   Decinosity   Decinosity   Decinosity   Decinosity   Decinosity   Decinosity   Decinosity   Decinosity   Decinosity   Decinosity   Decinosity   Decinosity   Decinosity   Decinosity   Decinosity   Decinosity   Decinosity   Decinosity   Decinosity   Decinosity   Decinosity   Decinosity   Decinosity   Decinosity   Decinosity   Decinosity   Decinosity   Decinosity   Decinosity   Decinosity   Decinosity   Decinosity   Decinosity   Decinosity   Decinosity   Decinosity   Decinosity   Decinosity   Decinosity   Decinosity   Decinosity   Decinosity   Decinosity   Decinosity   Decinosity   Decinosity   Decinosity   Decinosity   Decinosity   Decinosity   Decinosity   Decinosity   Decinosity   Decinosity   Decinosity   Decinosity   Decinosity   Decinosity   Decinosity   Decinosity   Decinosity   Decinosity   Decinosity   Decinosity   Decinosity   Decinosity   Decinosity   Decinosity   Decinosity   Decinosity   Decinosity   Decinosity   Decinosity   Decinosity   Decinosity   Decinosity   Decinosity   Decinosity   Decinosity   Decinosity   Decinosity   Decinosity   Decinosity   Decinosity   Decinosity   Decinosity   Decinosity   Decinosity   Decinosity   Decinosity   Decinosity   Decinosity   Decinosity   Decinosity   Decinosity   Decinosity   Decinosity   Decinosity   Decinosity   Decinosity   Decinosity   Decinosity   Decinosity   Decinosity   Decinosity   Decinosity   Decinosity   Decinosity   Decinosity   Decinosity   Decinosity   Decinosity   Dec | IYKGVI QAI QKSDEGHPPRAYLESEVAI SEEL VQKYSNSALGHVNSTIKELRILPI VDDL                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              | ò          | PAAPAAPBRO                                                       |
| 106 PSWER   106 PSWER   106 PSWER   106 PSWER   106 PSWER   106 PSWER   106 PSWER   106 PSWER   106 PSWER   106 PSWER   106 PSWER   106 PSWER   106 PSWER   106 PSWER   106 PSWER   106 PSWER   106 PSWER   106 PSWER   106 PSWER   106 PSWER   106 PSWER   106 PSWER   106 PSWER   106 PSWER   106 PSWER   106 PSWER   106 PSWER   106 PSWER   106 PSWER   106 PSWER   106 PSWER   106 PSWER   106 PSWER   106 PSWER   106 PSWER   106 PSWER   106 PSWER   106 PSWER   106 PSWER   106 PSWER   106 PSWER   106 PSWER   106 PSWER   106 PSWER   106 PSWER   106 PSWER   106 PSWER   106 PSWER   106 PSWER   106 PSWER   106 PSWER   106 PSWER   106 PSWER   106 PSWER   106 PSWER   106 PSWER   106 PSWER   106 PSWER   106 PSWER   106 PSWER   106 PSWER   106 PSWER   106 PSWER   106 PSWER   106 PSWER   106 PSWER   106 PSWER   106 PSWER   106 PSWER   106 PSWER   106 PSWER   106 PSWER   106 PSWER   106 PSWER   106 PSWER   106 PSWER   106 PSWER   106 PSWER   106 PSWER   106 PSWER   106 PSWER   106 PSWER   106 PSWER   106 PSWER   106 PSWER   106 PSWER   106 PSWER   106 PSWER   106 PSWER   106 PSWER   106 PSWER   106 PSWER   106 PSWER   106 PSWER   106 PSWER   106 PSWER   106 PSWER   106 PSWER   106 PSWER   106 PSWER   106 PSWER   106 PSWER   106 PSWER   106 PSWER   106 PSWER   106 PSWER   106 PSWER   106 PSWER   106 PSWER   106 PSWER   106 PSWER   106 PSWER   106 PSWER   106 PSWER   106 PSWER   106 PSWER   106 PSWER   106 PSWER   106 PSWER   106 PSWER   106 PSWER   106 PSWER   106 PSWER   106 PSWER   106 PSWER   106 PSWER   106 PSWER   106 PSWER   106 PSWER   106 PSWER   106 PSWER   106 PSWER   106 PSWER   106 PSWER   106 PSWER   106 PSWER   106 PSWER   106 PSWER   106 PSWER   106 PSWER   106 PSWER   106 PSWER   106 PSWER   106 PSWER   106 PSWER   106 PSWER   106 PSWER   106 PSWER   106 PSWER   106 PSWER   106 PSWER   106 PSWER   106 PSWER   106 PSWER   106 PSWER   106 PSWER   106 PSWER   106 PSWER   106 PSWER   106 PSWER   106 PSWER   106 PSWER   106 PSWER   106 PSWER   106 PSWER   106 PSWER   106 PSWER   106 PSWER   106 PSWER   106 PSWER   106  |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                | qq         |                                                                  |
| 116   12   12   13   13   13   13   13   13                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                | ò          | PSWERSPAAPAPSLPPAAAVLPSKLPEDD                                    |
| 135                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                | qq         | TTFDRKGPLTIPEEVEKAAAAQNNDLDDFDPLVTSNTGAAFGAAVGAAAV-              |
| Db   2224 MFGHQKFETVPRPPTP                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                | Võ         |                                                                  |
| Oy   167                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                | qq         | MFGHQKFETVPRPPTPP                                                |
| Db 2280 IDPKTVPPCAQNARSPGEIMFLIAFFVYLSCFASFFSKSLPLINILSLIVH  Cy 167                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                | ò          |                                                                  |
| Cy   167                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     | 215<br>otherical profein WOGA7 3a - Caenorhabditis elegans                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     | qa         | IDFKTVPPCAQNAFSPGEIMFLLAFFVYLSCFASFFSKSLPLLDNLLSLVVYLSISLIIH     |
| De 2140 VKHHRKFRNNEGATTMSKLGAVGRGLYALIAPIVNIVLRVGLNVALLVVGVAVSANEATYK  Data Library, August 1996  translated from GB/EMBL/DDBJ  QY 221 SFRIYKGVIQAIQKSDEGHPRAYLESEVAISELLVLFVVTYSLLIALGAAA  QY 221 SFRIYKGVIQAIQKSDEGHPRAYLESEVAISELLVGKYSNSALGHVNSTIKELRRLFLV  LID  ALO  210 STRIYKGVIQAIQKSDEGHPRAYLESEVAISELLVGKYSNSALGHVNSTIKELRRLFLV  QY 221 SFRIYKGVIQAIQKSDEGHPRAYLESEVAISELLVGKYSNSALGHVNSTIKELRRLFLV  QY 221 SFRIYKGVIQAIQKSDEGHPRAYLESEVAISELLVGKYSNSALGHVNSTIKELRRLFLV  QY 221 SFRIYKGVIQAIQKSDEGHPRAYLESEVAISELLVGKYNSTIKELRRLFLV  QY 221 SFRIYKGVIQAIQKSDEGHPRAYLESEVAISELLVGKYNSTIKKGLVVV  QY 281 DDLVDSLKFAVLMWYTYVGALFKGLTLIALGLIGVFSVVFKKTOVDIPHIGANKS  1                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   | itis elegans<br>bemiente ravision 15-Ort-1999 #text rhange 09-                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 | ò          |                                                                  |
| Data Library, August 1996  Data Library, August 1996  Cy 167RGSGSSVVDLLYWRDIKKTGVVFGASLFLLLSLTVPSIVSVTAYIALALLSVTI                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           | NO DESCRIPTION OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY | qq         |                                                                  |
| Db   2400 LTKSSGVLRKKEVLDVIVWRDAKKSAIVLSTALLVLYVTYSLLLALGAAA     Li                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          | Data Library, August                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           | ò          | RGSGSSVVDLLYMRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTI           |
| Cy   221 SFRIYKGVIOAIQKSDEGHPFRAYLESEVAISELVQKYSNSALGHVNSTIKELRRLFLV   L                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     | translated from                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                | q          |                                                                  |
| Second Formation                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             | TI.>                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           | ò          | SFRIYKGVIQAIQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELFLV        |
| Oy 281 DDLVDSLKFAVLAWWVFTVGALFNGLTLLILALISLFSIPVIYERHQVOIDHYLGIAANKS    1                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    | 112.<br>112. 123187; EMBL: 278066; PIDN: CAB01522.2; GSPDB: GN00023;                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           | gg         |                                                                  |
| Db 2520 ESPLESIKFGLVIMSLTVIASWFSGFTLAILGLGVFSVPKVYESNQEAIDPHLATISGH  1. 1866/3; 1963/3; 1990/3; 2262/1; 2289/1; 2462/2; 2586/2  2. 186/3; 1963/3; 1990/3; 2262/1; 2289/1; 2462/2; 2586/2  2. 186/3; 1963/3; 1990/3; 2262/1; 2462/2; 2586/2  Qy 341 VKDAMAKIQARK 356  2. 187; Score 427.4; DB 2; Length 2607;  Db 2580 LKNVQNIIDEKLPFLR 2595  Conservative 78; Mismatches 137; Indels 686; Gaps 21;  RENIT 6                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  | Appendical bource: close mosa.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 | ò          | DDLVDSLKFAVLMWVFTYVGALFNGLTLILALISLFSIPVIYERHQVQIDHYLGLANKS      |
| ch 23.4%; Score 427.4; DB 2; Length 2607; Db 25.4%; Score 427.4; DB 2; Length 2607; Db 25.80 LKNVQNIIDEKLPFLR 135; Conservative 78; Mismatches 137; Indels 686; Gaps 21; RESULT 6                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            | om/.3a<br>/5<br>/5 1866/3: 1967/3: 1990/3: 2262/1: 2289/1: 2412/1: 2462/2:                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     | q          |                                                                  |
| 23.4%; Score 42/.4%; Db 2580 LKNVQNIDEKLPFLR 5; Conservative 78; Mismatches 137; Indels 686; Gaps 21; MPDIDOSTVSSST                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                | ò          | VKDAMAKIQAKIPGLK                                                 |
| MEDITOOSSIVSSSTVSSST14                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       | 23.4%; Score 427.4; DB 2; Length 2607;<br>Similarity 13.0%; Pred. No. 3.8e-05;<br>Si Conservative 78; Mismatches 137; Indels 686; Gaps                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         | ą          | : :<br>LKNVQNIIDEKLPFLR                                          |
|                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              | WEDTDOSSIVSSSTVSSST.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           | P.ESIT.T   | 400                                                              |

В. Г.,

```
A; Molecule type: mRNA
A; Residues: 417-490
 A; Roberte type: mRNA
 A; Residues: 417-490
 A; Residues: 417-490
 A; Cross-references: GB:M14280; NID:g212607; PIDN:AAA49039.1; PID:g212608
 A; Cross-references: GB:M14280; NID:g212607; PIDN:AAA49039.1; PID:g212608
 A; Cross-references: GB:M14280; NID:g212607; PIDN:AA49039.1; PID:g212608
 B; Birnbaumer, M.; Hinrichs-Rosello, M.V.; Cook, R.G.; Schrader, W.T.; O'Malley, B.W.
 Mol. Endocrinol. 1, 249-259, 1987
 A; Reference number: A40911; MUD:88288199; PMID:3453892
 A; Reference number: A40911; MUD:88288199; PMID:3453892
 A; Residues: protein
 A; Residues: 128-133, 'E', 135-147, 'E', 149-164;546-558
 A; Residues: 128-133, 'E', 135-147, 'E', 148-164;546-558
 B; Simpson, R.J.; Grego, B.; Govindan, M.V.; Gronemeyer, H.
 Mol. Cell. Endocrinol. 52, 177-184, 1987
 A; Title: Peptide sequencing of the chick oviduct progesterone receptor form B.
 A; Reference number: A61552; MUID:88005426; PMID:3653503
 A; Accession: A61552; MUID:88005426; PMID:3653503

 residue 21
R.J.; Garni
 R.G.; Maxwell,
 28;
 A; Molecule type: mRNA
A; Residues: 126-133, 'E', 135-147, 'E', 149-164 <CO2>
A; Note: the authors translated the codon CAG for residue 7 as Glu and CAG for A; Note: the authors translated the codon CAG for residue 7 as Glu and CAG for R; Jeltsch, J.M.; Krozowski, Z.; Quirin-Stricker, C.; Gronemeyer, H.; Simpson, Proc. Natl. Acad. Sci. U.S.A. 83, 5424-5428, 1986
A; Title: Cloning of the chicken progesterone receptor.
A; Reference number: A24312; MUID:86287271; PMID:2426697
 117
 357
 48
 65
 88
 298 VGLPAAPPPFLGAKAAPADFAQPPRAGQEPSLECVLYKAEPPLLPGAYGPPAAPDSLPST
 49 EDLEELEVLER------KPAAG-----LSAAAVPPAAAAPLLDFSSD--SVPP
 66 QORBEBEBEBEBEDRDCPSYRPGGGSLSKDCLDSVLDTFLAPAAHAAPWSLFGPEVPEVPV
 126 APMSRGPEQKAVDAGPGAPGPSQP----RPGAPLWPGADSLNVAVKARPGPEDASENRAP
 182 GLPGAEERGFPERDAGPGGGGLAPAAAASPAAV----EPGAGQDYLHVPILPLNSAFLAS
 238 RTROLLDVEAAYDGSAFGPRSSPSVPAADLAEYGYPPPDGKEGPFAYGEFQSALKIKEEG
 -----FKYQFVTEPEDEEDEEEEEDEEDD
 A Molecule type: protein

A Molecule type: protein

A Residues: 136-153;168-174;195-228;526-537,'X',539;546-563 <SIM>
C;Genetics:
A;Introns: 400/2; 451/1; 490/1; 591/1; 639/2; 683/1; 735/3

A;Introns: 400/2; 451/1; 490/1; 591/1; 639/2; 683/1; 735/3

C;Superfamily: progesterone receptor; erbA transforming protein homology
C;Keywords: DNA binding; nucleus; steroid hormone receptor; zinc finger
F;1-786/Product: progesterone receptor form B #status predicted <AA1>
F;128-786/Product: progesterone receptor form A #status predicted <AA2>
F;491-682/Domain: erbA transforming protein homology <BRBA>
F;421-441/Region: zinc finger
 A, Residues: 1-64, E, 65-786 < CON>
A; Cross-references: GB:M37518
R; Connealy, O.M.; Sullivan, W.P.; Toft, D.O.; Birnbaumer, M.; Cook, Science 233, 77-70, 198
A; Title: Molecular cloning of the chicken progesterone receptor.
A; Reference number: A24661; MUID:86289413; PMID:2426779
 469;
 118 SLP-------PAAAVLPSKLPEDDEP--------
 14.9%; Score 272.1; DB 2; Length 715.9%; Pred. No. 0.36;
tive 54; Mismatches 119; Indels
 89 AP--RGP----LPAAPPAAPERQPSWERSPAAP-
 11 SSSTDSPP------RPPPA----
 121; Conservative
 Similarity
 A;Accession: A24661
 Query Match
Best Local S:
Matches 121
 g
 원
 g
 g
 ð
 셤
 ò
 ò
 ò
 Ś
 A;Residues: 1-222 <WIL>
A;Cross-references: UNIPROT:Q23188; EMBL:Z78066; PIDN:CAB01523.1; GSPDB:GN00023; CESP:WG
 Ξ
 A,Title: The chicken progesterone receptor: sequence, expression and functional analysis
A,Reference number: S06284; MUID:88166640; PMID:3443098
 A;Cross-references: UNIPROT:P07812; GB:M32732; GB:J05240; NID:g212554; PIDN:AAA49011.1; R;Gronemeyer, H.; Turcotte, B.; Quirin-Stricker, C.; Bocquel, M.T.; Meyer, M.E.; Krozow
 C.S.;
 progesterone receptor form B - chicken
N;Contains: progesterone receptor form A
C;Species: Gallus Gallus (chicken)
C;Date: 18-Nov-1994 #text_change 09-Jul-2004
C;Accession: A35466; S06284; Ā40903; A24661; A24312; A40911; A61552
R;Jeltsch, J.M.; Turcotte, B.; Garnier, J.M.; Lerouge, T.; Krozowski, Z.; Gronemeyer, J. Biol. Chem. 265, 3967-3974, 1990
A;Title: Characterization of multiple mRNAs originating from the chicken progesterone A;Reference number: A35466; MUID:90154085; PMID:2303488
 A;Residues: 1.786 CMO>
A;Cross-references: EMBL:Y00092; NID:g63744; PIDN:CAA68282.1; PID:g63745
A;Cross-references: EMBL:Y00092; NID:g63744; PIDN:CAA68282.1; PID:g63745
B;Conneely, O.M.; Dobson, A.D.W.; Tsai, M.J.; Beattie, W.G.; Toft, D.O.; Huckaby, Mol. Endocrinol. 1, 517-525, 1987
A;Title: Sequence and expression of a functional chicken progesterone receptor.
A;Reference number: A40903; MUID:91042592; PMID:3183474
 'n
 223
 1YKGVIQAIQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRLFLVDDL 283
 284 VDSLKFAVLMWVFTYVGALFNGLTLLILALISLFSIPVIYERHQVQIDHYLGLANKSVKD 343
 77
 C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T26213
 104 RQPSWERSPAAPAPSLPPAAAVLPSKLPEDDEPPARPPPPPAGASPLAEPAAPPSTPAA
 164 PKRRGSGSSVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFR
 -----GKILDVIÝWRDAKKSAIVLSLALLVĽFVĽAKYPLLTVVTÝSLLLAĽGAAAGFR
 Gaps
 55;
hypothetical protein W06A7.3b - Caenorhabditis elegans C:Species: Caenorhabditis elegans
 18.5%; Score 337.5; DB 2; 25.7%; Pred. No. 0.0001; tive 49; Mismatches 84;
 A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
 submitted to the EMBL Data Library, August 1996
A;Reference number: Z20173
A;Accession: T26213
 KOPTW-----VPATDFP-----
 Experimental source: clone W06A7
 344 AMAKIQAKIPGLK 356
 | |:| |:
198 VQNIIDEKLPFLR 210
 Status: translation not shown
 Query Match
Best Local Similarity 25.74
Matches 65; Conservative
 A,Gene: CESP:W06A7.3b
A,Map position: 5
A,Introns: 27/1; 77/2; 201/2
 R;Gronemeyer, H.; Turcotte
EMBO J. 6, 3985-3994, 1987
 A, Residues: 1-786 <JEL>
 A; Molecule type: DNA
 A; Accession: A35466
 A; Accession: S06284
 224
 25
 13
 ઠે
 셤
 ద
 셤
 g
 à
 ò
 ò
```

ò

8 4 8 4 8 4 8 4 8 4 8 4

|                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                | Db 419 KARRERQRSGDPAPPDSPTWEAKKHRSRERKLGSHSTARRSRSRSRSRSRSRSADRRRG 478                                        |
|--------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|---------------------------------------------------------------------------------------------------------------|
|                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                | Qy 110 RSPAA 114                                                                                              |
| SAAFFGLYSFLGLNGHHQALGFPAAVLKEGLPQLCPPYIGYVRPDTETSQSSQYSFESLP                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   |                                                                                                               |
| ONT OF TAXOBER COMMUNITY BACKGRANDER AND ALTERNATIVE COMMUNITY BACKGRANDER COMMUNITY COMMUNITY COMMUNITY COMMUNITY COMMUNITY COMMUNITY COMMUNITY COMMUNITY COMMUNITY COMMUNITY COMMUNITY COMMUNITY COMMUNITY COMMUNITY COMMUNITY COMMUNITY COMMUNITY COMMUNITY COMMUNITY COMMUNITY COMMUNITY COMMUNITY COMMUNITY COMMUNITY COMMUNITY COMMUNITY COMMUNITY COMMUNITY COMMUNITY COMMUNITY COMMUNITY COMMUNITY COMMUNITY COMMUNITY COMMUNITY COMMUNITY COMMUNITY COMMUNITY COMMUNITY COMMUNITY COMMUNITY COMMUNITY COMMUNITY COMMUNITY COMMUNITY COMMUNITY COMMUNITY COMMUNITY COMMUNITY COMMUNITY COMMUNITY COMMUNITY COMMUNITY COMMUNITY COMMUNITY COMMUNITY COMMUNITY COMMUNITY COMMUNITY COMMUNITY COMMUNITY COMMUNITY COMMUNITY COMMUNITY COMMUNITY COMMUNITY COMMUNITY COMMUNITY COMMUNITY COMMUNITY COMMUNITY COMMUNITY COMMUNITY COMMUNITY COMMUNITY COMMUNITY COMMUNITY COMMUNITY COMMUNITY COMMUNITY COMMUNITY COMMUNITY COMMUNITY COMMUNITY COMMUNITY COMMUNITY COMMUNITY COMMUNITY COMMUNITY COMMUNITY COMMUNITY COMMUNITY COMMUNITY COMMUNITY COMMUNITY COMMUNITY COMMUNITY COMMUNITY COMMUNITY COMMUNITY COMMUNITY COMMUNITY COMMUNITY COMMUNITY COMMUNITY COMMUNITY COMMUNITY COMMUNITY COMMUNITY COMMUNITY COMMUNITY COMMUNITY COMMUNITY COMMUNITY COMMUNITY COMMUNITY COMMUNITY COMMUNITY COMMUNITY COMMUNITY COMMUNITY COMMUNITY COMMUNITY COMMUNITY COMMUNITY COMMUNITY COMMUNITY COMMUNITY COMMUNITY COMMUNITY COMMUNITY COMMUNITY COMMUNITY COMMUNITY COMMUNITY COMMUNITY COMMUNITY COMMUNITY COMMUNITY COMMUNITY COMMUNITY COMMUNITY COMMUNITY COMMUNITY COMMUNITY COMMUNITY COMMUNITY COMMUNITY COMMUNITY COMMUNITY COMMUNITY COMMUNITY COMMUNITY COMMUNITY COMMUNITY COMMUNITY COMMUNITY COMMUNITY COMMUNITY COMMUNITY COMMUNITY COMMUNITY COMMUNITY COMMUNITY COMMUNITY COMMUNITY COMMUNITY COMMUNITY COMMUNITY COMMUNITY COMMUNITY COMMUNITY COMMUNITY COMMUNITY COMMUNITY COMMUNITY COMMUNITY COMMUNITY COMMUNITY COMMUNITY COMMUNITY COMMUNITY COMMUNITY COMMUNITY COMMUNITY COMMUNITY COMMUNITY COMMUNITY COMMUNITY COMMUNITY COMMUNITY COMMUNITY COMMUNITY COMMUNITY COMMUNITY COMMUNITY COMMUNITY C | Qy 115PAPSLP                                                                                                  |
| QALCELICGDEASGCHTGVICGSCKVFFKRAMEGQHNTLCAGRNDCLVDKLRRKNCPACR                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   |                                                                                                               |
| WEDIKKTGVVFGASLFLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQAIQAIQKSDEG                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 | Qy 126 LpS 128                                                                                                |
| LEKACCQAGMVLGGGKKFKKLIN                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        | DD 599 SPKGEVLYDSEGLSADERGAKGDKDRRRSGAASSSSSREKASRRKALDGDRGRDRDRSS 658                                        |
| HPFKAYLESEVAISEELVQXXSNSALGHVNSTIKELR                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          | Qy 129KLPEDDEP 136                                                                                            |
| AVLQDBTQSLTQRLSFSPNQBIPFVPPMISVLRGIBPEVVYAGYDNTKPETPS                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          | Db 659 KKPRTPKDSAPGSGALPKAPPRSGSSSSSSSSSKVKVKLQSKVAVLIREGVSSTTPAKDS 718                                       |
|                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                | Qy 137 136                                                                                                    |
| SUBJECTANDUCERQUECTVVANSALDERGFRANDHIDUQITLLQISSWASTNSD                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        | Db 719 SSSGLGSIGVKFSRDRESRSPFLKPDERSPAEGVKVAPGSTKPKKTKAKAKAKAGAKKAKGT 778                                     |
| SUS INTERMEDIATION OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROP | Qy 137                                                                                                        |
| TOTAL CONTROLLED TO CONTROLLED AND CONTROLLED AND AND AND AND AND AND AND AND AND AN                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           | Db 779 KGKTKPSKTRKKVRSGGSSTASGGPGSLKKSKADSCSQAASAKGTEETSWSGEERTTKAP 838                                       |
| 534 LT                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         | Qy 138 ARPP145                                                                                                |
|                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                | Db 839 STPPPKVAPPPPALTPDSQTVDSSCKTPDVSFLABEASEDTGVRVGAEBEBEBEBEBEB 898                                        |
| SULT 8                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         | Qy 146 AGASPLAEPAA                                                                                            |
| -77                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            | Db 899 EEQQPATTTATSTAAAAPSTAPSAGSTAGDSGAEDGPAARASQLPTLPPPMPWNLPAGVD 958                                       |
| Species: Marcus Morveylous (Norway rat)  19-0ct-1999 #sequence_revision 29-0ct-1999 #text_change 09-Jul-2004                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   | Qy 157 160                                                                                                    |
| Accession: 131421<br>Yuryev, A.; Patturajan, M.; Litingtung, Y.; Joshi, R.V.; Gentile, C.; Gebara, M.; Cord                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    | DD 959 CTTSGVLALTALLFKMBEANLASRAKAQELIQDTNQILRHRKPPSTLGVTPAPVPTSFGL 1018                                      |
| OC: Natl. Acad. Scl. 0.5.A. 95, 6975-6980, 1996 Title: The C-terminal domain of the largest subunit of RNA polymerase II interacts wit                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         | Qy 161                                                                                                        |
| Reference number: Azioza; muid:96293439; Fmid:0092925                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          | Db 1019 PPAPSSYLLPGSLPIGGCGSTPPTPTGLVPASDKREGSSSS 1059                                                        |
| Status: preliminary; tramslated from GB/EMBB/DDBS<br>Docidioc, 1-112 -VTB.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     | Qy 192 SLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQAIQKSDEGHPFRAYLESEVAI 251                                       |
| Negaruces: 1-11.3 VIONA<br>TOOSs-references: UNIPROT:063624; EMBL:U49056; NID:g1438531; PID:g1438532; PIDN:AAC526<br>Experimental source: himocampus                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           | Db 1060 1062                                                                                                  |
| Match Courses 17 CF.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           | QY 252 SEELVQKYSNSALGHVNSTIKELRLVDDLVDSLKFAVLMWVFTYVGALFNGLTLIL 311                                           |
| Similarity 98%; Pred. No. 1.4;<br>Consourselve 32. Mismatches 60. Indels 061.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  | Db 1063 GDTDKYLKKLHTQERAVEEVK1083                                                                             |
| TIO; COMBETVACIVE 32; MIRMACCHES 09; IMCETS 901; GADS                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          | Qy 312 ALISLFSIPVIYERHQVQIDHYLGLANKSVKDAMAKIQAKI352                                                           |
| SSSTDSPERPPKTQKTQ                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              | Db 1084LSIKPYYQKKDITKEEYKDILRKAVHKICHSKSGEINPVKVSNLVRA 1130                                                   |
| SSSSPSPPPPPPPPPPPPALPAPRFDIXDPFHPTDEAXSPPPAPEQRXDPFEATGSNPSSS                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  | Qy 353PGL 355                                                                                                 |
| 28 -FVTERPDENDENEREREENER                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      | Db 1131 YVQRYRYFRKHGRKPGDPPGPPRPPKEPGPPDKGGPGL 1168                                                           |
| <u> </u>                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       |                                                                                                               |
| LGAPGTPPQADSTRAEGAPRRRVFVVGPEAEACLEGKVSVEVVTTAGGPALPLPPTD                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      | tical protein SPAC23A1.17 - fission yeast (Schizosaccharces: Schizosaccharomyces pombe                        |
| 49 EDLEELEVIE                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  | C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_cnange 09-Ju1-2004<br>C;Accestor T38236              |
| DFSSDSRGPLPAAPPA                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               | submitted to the EMBL Data Library, February 1998<br>A,Reference number: 221780<br>A,Accession: T3826         |
| 359 SLHADSDGEGALQVDLGEPPAPPAADARWGGLDLRRKILTQRRERYRQRSASPGPPPARK 418 101APEROPSWE109                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           | A;Status: preliminary; translated from GB/EMBL/DDBJ<br>A;Molecule type: DNA<br>A;Residues: 1-1611 <mnr></mnr> |
|                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                | A, Cross-references: UNIPROT: 042854; EMBL: AL021813; PIDN: CAA16991.1; GSPDB: GN00066; SPDB:                 |

6 B 6 B 6 B 6 B 6

|                                                                                                                                                                                                                                                                   | RESULT 10  Til 286  Captucino gene protein - fruit fly (Drosophila melanogaster)  C.Species: Drosophila melanogaster  C.Species: Drosophila maternal effect rene required for polarity of strictic: Capuccino, a Drosophila maternal effect rene required for polarity of A.Title: Capuccino, a Drosophila maternal effect rene required for polarity of A.Scatus: prelliminary: translated from GB/EMBL/DDBJ  A.Scatus: prelliminary: translated from GB/EMBL/DDBJ  A.Molecule type: mRNA  A.Residues: 11058 < EMM>  A.Residues: 11058 < EMM>  A.Residues: 11058 < EMM>  A.Gross-references: PlyBase: FBgn0000256  Query Watch  G.Gene: capu  A.Gross-references: PlyBase: FBgn0000256  Query Watch  Best Local Similarity 16.2%; Pred. NO. 2.1;  Matches 114; Conservative 51; Mismatches 103; Indels 435; Gaps 27;  Matches 114; Conservative 51; Mismatches 103; Indels 435; Gaps 27;  A. Indels 114; Conservative 51; Mismatches 103; Indels 435; Gaps 27;  A. Indels 114; Indels 114   Indels 114   Indels 114   Indels 114   Indels 114   Indels 114   Indels 114   Indels 114   Indels 114   Indels 114   Indels 114   Indels 114   Indels 114   Indels 114   Indels 114   Indels 114   Indels 114   Indels 114   Indels 114   Indels 114   Indels 114   Indels 114   Indels 114   Indels 114   Indels 114   Indels 114   Indels 114   Indels 114   Indels 114   Indels 114   Indels 114   Indels 114   Indels 114   Indels 114   Indels 114   Indels 114   Indels 114   Indels 114   Indels 114   Indels 114   Indels 114   Indels 114   Indels 114   Indels 114   Indels 114   Indels 114   Indels 114   Indels 114   Indels 114   Indels 114   Indels 114   Indels 114   Indels 114   Indels 114   Indels 114   Indels 114   Indels 114   Indels 114   Indels 114   Indels 114 |  |
|-------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|-------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|--|
| A; Experimental Bource: strain 972h-; cosmid c23Al C; Genetics: A; Gene: SPDB:SPAC23Al.17 A; Map position: 1 Query Match Best Local Similarity 10.1%; Pred. No. 3.4; Matches 131; Conservative 59; Mismatches 106; Indels 1005; Gaps 30; Qy 2 EDIDQSSLVSSSTDSPPRP | 479 PPKDSSSTSTQPTEQSNAQQAPSPKEEERPLPSEPSQNQPAEYRDTPDTPRNIMPLPGLM                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              |  |

```
ect rene required for polarity of the egg \epsilon:0:7590229
 8; NID:g1061333; PID:g1061334; PIDN:AAC4692
 GQDKKYKSVHILFPDYSQTVLTATFNPH 1430
 ERHETSTSSRKSSKSGEHHHHHNEGHAD 1317
 SRASKKPSIVSTTGPFNESFSAKPVEPC 1370
 ------ viv 1509
 P----- SIVSVIAYI----- 211
 LVQK----YSNSALGHVNSTIKELRRLF 278
 -----FNGLTLLILALISLFSIPVIY 323
 KTLQQILKKRLLNCSTLAEVHAVVNELL 399
 S----- LPPAAAVLPSK----- 129
 : |||
APIEGGGGIPPPPPMSASPSKTTISPA 566
 DLLYWRDIKKT----- 185
 | :|::|
---IWTEIEETPLDNIDEFTELFSRQAI 675
-----RGS 169
 -----ARPPPPP------AG 147
 -----VTEPEDEEDEEEEDEE---- 45
 AGLSAAAVPPAAAAPLLDFSSDSVPPAP 90
 1999 #text_change 09-Jul-2004
 .1;
se 103; Indels 435; Gaps
 James, B.; Manseau, L.
 DB 2; Length 1058;
 a melanogaster)
 EPINKQTFGG----
 IQAKIPGLK 356
 י/ססשת
```

| Db 746LDFLELLMRFLPTEYERSLITRFEREQRPMEELSEEDRFMLCFSRIPRLPERMTTLT 802  Qy 298 YVGALPNGLTLLITALISL | REBUILT 12   STACE                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             |
|-------------------------------------------------------------------------------------------------|--------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
|                                                                                                 | RESULT 11  LOURONCE (Comin protein - human Captens (man)   Capecies: Howen septens (man)   Capecies: Howen capecies (man)   A; Reaston (man)   A; Reaston (man)   A; Reaston (man)   Capecies: Man   Capecies: Howen capecies (man)   Capecies (man)   Capecies (man)   Capecies (man)   Capecies (man)   Capecies (man)   Capecies (man)   Capecies (man)   Capecies (man)   Capecies (man)   Capecies (man)   Capecies (man)   Capecies (man)   Capecies (man)   Capecies (man)   Capecies (man)   Capecies (man)   Capecies (man)   Capecies (man)   Capecies (man)   Capecies (man)   Capecies (man)   Capecies (man)   Capecies (man)   Capecies (man)   Capecies (man)   Capecies (man)   Capecies (man)   Capecies (man)   Capecies (man)   Capecies (man)   Capecies (man)   Capecies (man)   Capecies (man)   Capecies (man)   Capecies (man)   Capecies (man)   Capecies (man)   Capecies (man)   Capecies (man)   Capecies (man)   Capecies (man)   Capecies (man)   Capecies (man)   Capecies (man)   Capecies (man)   Ca |

```
A,Experimental source: clone Y48B6A
Genetics:
A,Gene: CESP:
A,Introns: 38/3; 196/3; 437/2; 460/3; 518/1; 617/3; 673/3
 283
 96
 122
 463
 Query Match
 time
 Search
Job tim
 셤
 ò
 유
 8
 g
 ઠે
 a
 ď
 ઠે
 셤
 셤
 셤
 ò
 ò
 à
 셤
 ઠે
 8
 A;Accession: S11515
A;Molecule type: mRNA
A;Residues: 1-1468 <WOY>
A;Cross-references: UNIPROT:Q05860; EMBL:X53599; NID:g52877; PIDN:CAA37668.1; PID:g52878
 A,Cross-references: UNIPROT:Q9U2A6; EMBL:AL110490; NID:e1542263; PIDN:CAB54442.1; CESP:M
 -----IOI 1005
 1006 NDKSQDAAPTLWDSLEEPHIRDTSEFEYLFSKDTTQQKKKPLSEAYEKKNKVKKIIKLLD 1065
 9601 S-----
 |: | |: | CPFLLHEKEKTSRSELYLDIANPDQSPTEQDDRTPGRLQAVWPPPKTKDTEEKVGLKYTE 721
 944
 997
 257
 258 -KYSNSA---LGHVNSTIKELRR-LFLVDDLVDSLKFAVLMWVFTYVGALFNGLTLLILA 312
 EEASEKGLGPEKITAPPQHQLPPGIASEGFPCDNFKEQTAKDLPNKDGGVWVPGYRAGPP 661
 722 AEYQAAILHLKREHKEEIETLQAQFELKTFHIRGEHALVTARLEEAIENLKQQLEKRREG 781
 782 CEEMRDVCISTDDDCSPKAFRNVCIQTDRETFLKPCDAESKATRSSQIVPKKLTISLTQL 841
 842 SPSKDSKDIHAPFQTREGTSSSSQQKISPPAPPTPPPLPPPL-----IPPPPLPPGL 894
 --PSTPAAPKRGSGS 171
 SVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQA 231
 48
 91
 hypothetical protein Y48B6A.6 - Caenorhabditis elegans
C,Species: Caenorhabditis elegans
C,Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
 GPLPPAPPIPPV-----CPVSPPPPPPPP---PTPVPPSDGPPPPPPPNVLA
 -----VPPAAAAPLLDFSSDSVPPAP----R
 GPLPAAPPAAPERQPSWERSPAAPAPSLPPAAAVLPSKLPEDDEPPARPPPPPP----
 Gaps
 431;
 DB 2; Length 1468;
 Indels
 LISLFSIPVIYERHQVQIDHYLGLANKSVKDAMAKIQ------
Reference number: $11515; MUID:90363291; PMID:2392150
 40; Mismatches 103;
 EDIDOSSLVSSSTDSPPRP--PPA------FKYQ-
 Accession: T26998
Status: preliminary; translated from GB/EMBL/DDBJ
Molecule type: DNA
 232 IQKSDEGHP------FRAYLESEVAISEELVQ-
 submitted to the EMBL Data Library, September 1999
 Score 254.9; D
Pred. No. 6.3;
 --FVTEPEDEEEEE------EDEEEDD
 Query Match
Best Local Similarity 14.5%;
Matches 97; Conservative 4
 LAQIPNFAERA 1154
 -AKIPGLKRKA 359
 ----LYWTR----
 A;Reference number: Z20297
 -716 <WIL>
 Accession: T26998
 1144
 602
 146
 172
 966
 49
 9
 70
 8
 895
 313
 g
 g
 g
 <u>අ</u>
 ò
 a
 ઠે
 셤
 ઠે
 ò
 δ
 셤
 셤
 δ
 엄
 ò
 ð
 유
 8
 유
 요
 ઠે
 ò
 ŝ
```

```
23;
 282
 403 LPPPPPPFKPETPLAIRRAGPIPTPQLLEMIHQEDCSIRPSSPTSVSHGSRPQSPAVPKKP 462
 248
 237
 -----AAPPAAPERQPSWE------121
 PSPRPTSVPPPIPSPGPSEDVNMDELIESFSDSVIFNNSMSPPPPLPPLRESSLETLEVT 342
 167
 -----SVTVSPLGLLC 473
 ----- FRIYKGVIQAI - 232
 474 DPNLSIEKPEEMKTEDTKPVETAPAPVDEAELNDALDRRNKINEATCLTKIFPSLVSKYF 533
 534 QNCSFDFLNDKRSGENVPLKMNKKISLYAEFSEFSRKQIQYFSGIFKKYDEDQDSYIDFN 593
 ------VAISEELVQKYSNSALGHVNSTIKELRRLFLVDDLVDSLKFAVLM 293
 343 PEDPVTESKVEASPTPLPKATESLNESSIKALEGLEVKALEAQEASDDRPSAPTPIRDSS 402
 95
 294 WVFTYVGALFNGLTLLILALISLFSIPVIYERHQVQIDHYLGLANKSVKDAMAKIQAKI 352
 5 DOSSLVSSSTD-----SPPRPP-----PAFKYQFVTEPEDEEDEEEDEEDD
 ------FRAYLESE-----
 238 ASFEELEABIMRISRSP-----VPP----SIPPPPPPNIPLFIPQEVQSP
 168 GSGSSVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTIS----
 -----ESCSEVFK--TLAESVDVSKEGVLGAAN------FFQAKI
 Gaps
 353;
DB 2; Length 716;
 49 EDLEELEV----LERKPAAGLSAAAVPPAAAAPLLDFSSDSVPPAPRGPLP
 Indels
 39; Mismatches 106;
14.0%; Score 254.7; 16.9%; Pred. No. 1.1
 -----OKSDEGHP-----
 completed: June 23, 2005, 10:56:54
ne : 32.9653 secs
 RPPPPPAGASPLA-----
 ------AAAVLPSKLPE-
 Best Local Similarity 16.9
Matches 101; Conservative
```

This page Blank (Uspio)

Н

```
UNCTION
 RESULT 1
 mus musculu
mus musculu
 fasc
 xenopus lae
xenopus lae
 rattus norv
 homo sapien
 sapien
 xenopus tro
 xenopus lae
 xenopus lae
 June 23, 2005, 10:17:56; Search time 113.842 Seconds (without alignments) 1619.338 Million cell updates/sec
 mus musculu
 musculu
 mus musculu
 mus musculu
 musculu
 musculu
 gallus gall
 musculu
 xenopus lae
 taurus
 gallus gall
 scrofa
 scrofa
 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
 xenobna
 1823
1 MEDIDQSSLVSSSTDSPPRP......VKDAMAKIQAKIPGLKRKAD 360
 macaca
 homo
 Description
 8118
 Q8k3g7
Q8bgm9
Q8k3g8
Q9bgc3
Q6ipn0
Q8ipn0
Q8bgk7
Q8bgk7
 06jrv0
06jrv1
06jrv4
06jrv4
06jrv8
06jrv9
07t224
 Q6rss8
Q99p72
Q7yrw9
 Q6im70
Q6ify4
Q6ig15
 Q8bh78
Q8bh£5
 06 jrv2
 1612378
GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
 Total number of hits satisfying chosen parameters:
 1612378 seqs, 512079187 residues
 SUMMARIES
 Q96B16
RTN4 HUMAN
Q6IPN0
 OGRSSB
RTN4 MOUSE
Q7YRW9
 Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
 OM protein - protein search, using sw model
 Q8BHF5
Q8K3G7
 Q8BGM9
Q8K3G8
 Q80W95
Q8K290
 Q6IFY4
Q6IG15
Q7PCJ7
 QGJRV2
QGJRV0
QGJRV7
 28IUA4
 28BGK7
 DEIM70
 Gapop 10.0 , Gapext 0.1
 JEJRV1
 D6JRW1
 US-09-830-972-2-FUSED
 UniProt_03:*
1: uniprot_sprot:*
2: uniprot_trembl:*
 seq length: 0
seq length: 200000000
 Query
Match Length DB
 187
 1024
1043
1032
 311
 BLOSUM62
 Perfect score:
 1622.9
1598.4
1518.4
1471.5
1012.1
1010.2
992.2
988.7
 874.8
870.4
870.3
 Score
 Scoring table:
 896
 884.5
883.8
883.3
882.2
880.8
880.5
 1637
 900
 886.4
 1712.7
 1711.5
 899.1
 Minimum DB
Maximum DB
 Sequence:
 Searched:
 Database
 Run on:
 Š.
 Result
```

| Q6jrw2 xenopus lae |        |        | Q16799 homo sapien | Q8k0t0 mus musculu | Q8k4s4 mus musculu | Q64548 rattus norv | Q90638 gallus gall | Q6ify5 xenopus tro | Q6pb23 xenopus lae | Q6jrv6 xenopus lae | Q6jrw3 xenopus lae | Q6jrw4 xenopus lae | O7t222 carassius a |
|--------------------|--------|--------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|
| Q6JRW2             | Q7TNB7 | Q9GM33 | RIN1 HUMAN         | Q8K0T0             | Q8K4S4             | RIN1 RAT           | Q906 <u>3</u> 8    | QGIFYS             | Q6PB23             | QGJRV6             | Q6JRW3             | Q6JRW4             | Q7T222             |
| ď                  | ~      | ~      | н                  | ~                  | ~                  | ,                  | 7                  | ~                  | ~                  | N                  | ~                  | 7                  | 7                  |
| 316                | 720    | 179    | 116                | 780                | 780                | 111                | 760                | 193                | 199                | 193                | 199                | 193                | 214                |
| ٠,                 |        |        |                    |                    |                    |                    |                    |                    |                    |                    |                    |                    |                    |
| 47.2               | 46.9   | 46.3   | 45.3               | 45.3               | 45.2               | 44.3               | 43.5               | 42.4               | 42.0               | 41.7               | 40.9               | 40.8               | 40.4               |
|                    |        |        |                    |                    |                    |                    |                    |                    |                    |                    |                    |                    |                    |

## ALIGNMENTS

```
FUNCTION: Potent neurite outgrowth inhibitor which may also help block the regeneration of the nervous central system in adults (By
 STRAIN=Sprague-Dawley; TISSUE=Adipocyte;
MEDLINE=99249816; PubMed=10231557; DOI=10.1016/S0167-4889(99)00033-6;
MOTIES N.G., Ross S.A., Neveu J.M., Lane W.S., Lienhard G.B.;
"Cloning and characterization of a 22 kDa protein from rat adipocytes: a new member of the reticulon family.";
Biochim. Biophys. Acta 1450:68-76(1999).
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 similarity).

SUBCELLULAR LOCATION: Integral membrane protein. Anchored to the membrane of the endoplasmic reticulum through 2 putative transmembrane domains (By similarity).

ALTERNATIVE PRODUCTS:
 SEQUENCE FROM N.A. (ISOFORMS 2 AND 4).
STRAIN-WAISTER KYOLO, TISSUE-VASCUlar smooth muscle;
LTO T., Schwartz S.M.;
"Cloning of a member of the reticulon gene family in rat: one of two
 GrandPre T., Li S., Strittmatter S.M.; "Nogo-66 receptor antagonist peptide promotes axonal regeneration."; Nature 417:547-551 (2002).
 SEQUENCE FROM N.A. (ISOFORMS 1; 2 AND 3).
MEDLINE=20129258; PubMed=10667796; DOI=10.1038/35000219;
MEDLINE=20129258; PubMed=10667796; DOI=10.1038/35000219;
Spillmann A.A., Christ F., Schwab M.E.; Frank M., Schnell L.,
Spillmann A.A., Christ F., Schwab M.E.;
"Nogo-A is a myelin-associated neurite outgrowth inhibitor and an antigen for monoclonal antibody IN-1.";
Nature 403:434-439(2000).
ETN4 RAT STANDARD; PRT; 1163 AA.
O9JK11; Q9JK10; Q9R0D9; Q9WUE9; Q9WUF0;
28-FEB-2003 (Rel. 41, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
Reticulon 4 (Neurite outgrowth inhibitor) (Nogo protein) (Foocen)
 similarity).
SUBUNIT: Binds to RTN4R. Interacts with Bcl-xl and Bcl-2
 minor splice variants.";
Submitted (FEB-1999) to the EMBL/GenBank/DDBJ databases.
 MEDLINE=22033691; PubMed=12037567; DOI=10.1038/417547a;
 SEQUENCE FROM N.A. (ISOFORM 3), AND PARTIAL SEQUENCE
 Event-Alternative splicing; Named isoforms=4;
Name=1; Synonyms=Nogo-A, NI-220-250;
 Name=Rtn4; Synonyms=Nogo;
 Rattus norvegicus (Rat)
 NCBI_TaxID=10116;
```

~

```
.021 VIISFRIYKGVIQAIQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRL 1080
 FLVDDLVDSLKFAVLMMVFTYVGALFNGLTLLILALISLFSIPVIYERHQVQIDHYLGLA 337
 181 AASEPVIPSSAEKIMDLMEQPGNTVSSGQEDFPSVLLETAASLPSLSPLSTVSFKEHGYL 240
 301 AILVENTKEEVIVRSKDKEDLVCSAALHSPQESPVGKEDRVVSPEKTMDIFNEMOMSVVA 360
 721 PVDLFSDDSIPEVPQTQEEAVMLMKESLTEVSETVAQHKEERLSASPQELGKPYLESFQP 780
 841 IIDBFPTFVSAKDDSPKLAKEYTDLEVSDKSEIANIQSGADSLPCLELPCDLSFKNIYPK 900
 961 RSLSAVLSAELSKTSVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLLS
 241 GNLSAVSSSEGTIEETLNEASKELPERATNPFVNRDLAEFSELEYSEMGSSFKGSPKGES
 421 NEDASFPSTPEPVKDSSRAYITCASFTSATESTTANTFPLLEDHTSENKTDEKKIEERKA
 481 QIITEKTSPKTSNPFLVAVQDSEADYVTTDTLSKVTEAAVSNMPEGLTPDLVQEACESEL
 541 NEATGTKIAYETKVDLVQTSEAIQESLYPTAQLCPSFEEAEATPSPVLPDIVMEAPLNSL
 601 LPSAGASVVQPSVSPLEAPPPVSYDSIKLEPENPPPYEEAMNVALKALGTKEGIKEPESF
 781 NLHSTKDAASNDIPTLTKKEKISLQMEEFNTAIYSNDDLLSSKEDKIKESETFSDSSPIE
 901 DEVHVSDEFSENRSSVSKASISPSNVSALEPQTEMGSIVKSKSLTKEAEKKLPSDTEKED
 -----SVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLS
 VTISFRIYKGVIQAIQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRL
 361 PVREEYADFKPFEQAWEVKDTYEGSRDVLAARANVESKVDRKCLEDSLEQKSLGKDSEGR
 561 NAAVQETEAPYISIACDLIKETKLSTEPSPDFSNYSEIAKFEKSVPEHAELVEDSSPESE
 172 -----
 1141 NKSVKDAMAKIQAKIPGLKRKAD 1163
 NKSVKDAMAKIQAKIPGLKRKAD 360
 172 ----
 1081
 278
 172
 172
 218
 338
 172
 q
 g
 g
 à
 g
 a
 ò
 g
 g
 දු පු
 셤
 유
 ઠ
 ઠે
 8
 ò
 8
 ò
 g
 ò
 ద
 ò
 g
 셤
 ð
 ò
 . g
 ò
 q
 ò
 ద
 à
 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
 120
 9
 9
 Name=13 Synonymas-Nogo-C, VP20;

IsoId=Q9JK11-3; Sequence=VSP_005656, VSP_005657;

Name=4; Synonymas-Foocen-M2;

IsoId=Q9JK11-4; Sequence=VSP_005659;

TISSUE SPECIFICITY: Isoforms 1, 2 and 3 are present in optic

nerve, spinal cord and cerebral cortex. Isoforms 1 and 2 are

present in dorsal root ganglion, sciatic nerve and PC12 cells

after longer exposure. Isoforms 2 and 3 are detected in kidney,

cartilage, skin, lung and spleen. Isoform 3 is expressed at high

level in skeletal muscle. In adult animals isoform 1 is expressed
 PAAGLSAAAVPPAAAAPLLDFSSDSVPPAPRGPLPAAPPAAPERQPSWERSPAAPAPSLP
 MEDIDÓSSLVSSSTDSPPRPPPAFKYQFVTEPEDEEDEEBEBDEEDDEDLEBLEVLERK
 MEDIDQSSLVSSSTDSPPRPPPAFKYQFVTEPEDEEEEEDEEEDEEDDEDLEELEVLERK
 0; Indels 803; Gaps
 AVLSAELSKTS -> MDGQKKHWKDK (in isoform
 EMBL; AF0513135; AAF01564.1; -.
EMBL; AJ242961; CAB71027.1; -.
EMBL; AJ242962; CAB71028.1; -.
EMBL; AJ242962; CAB71029.1; -.
EMBL; AJ32046; AAD31019.1; -.
EMBL; AF132046; AAD31019.1; -.
EMBL; AF132046; AAD31020.1; -.
EMBL; AF132046; Caintegral to endoplasmic reticulum membrane; IDA.
GO; GO:000515; C:integral to endoplasmic reticulum membrane; IDA.
GO; GO:000515; F:protein binding; ISS.
GO; GO:0019987; P:negative regulation of anti-apoptosis; ISS.
GO; GO:0030517; P:negative regulation of axon extension; ISS.
 DB 1; Length 1163;
 Missing (In isoform 2).
/FTId-VSP_005658.
Missing (In isoform 4).
/FTId-VSP_005659.
Missing (In Ref. 3; AAD31020)
MW; 8CB894B09E94F0B6 CRC64;
 Cytoplasmic (Potential). Potential.
 Cytoplasmic (Potential)
Reticulon.
 Missing (in isoform 3) /FTId=VSP_005656.
 PROSITE; PS50845; RETICULON; 1.
Alternative splicing; Direct protein sequencing;
 Lumenal (Potential)
 Score 1732.7; DB 1
Pred. No. 1.2e-47;
0; Mismatches 0;
 FTId=VSP 005657
 mainly in the nervous system. SIMILARITY: Contains 1 reticulon domain
 Name=2; Synonyme=Nugu-b,IsoId=Q9JK11-2; Sequence=VSP_005658;
IsoId=Q9JK11-1; Sequence=Displayed;
 Potential
 Transmembrane.
 Poly-Ala
 Poly-Pro
 1130 1131 Mis
1163 AA; 126386 MW;
 95.0%;
31.0%;
 Best Local Similarity si.v
Matches 360; Conservative
 975
 975
 reticulum;
 Similarity
 192
 965
 Pfam; PF02453;
PROSITE; PS5084
 Endoplasmic r
DOMAIN
TRANSMEM 9
DOMAIN 11
TRANSMEM 11
DOMAIN 11
 CONFLICT
 VARSPLIC
 VARSPLIC
 Query Match
Best Local
 /ARSPLIC
 /ARSPLIC
 DOMAIN
```

480

171 900 99

171

1020

217

277

1140

g

셤 ò

ð

```
DDT TABLE TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL THE TOTAL TO THE TOTAL THE TO
 셤
 8
 셤
 ઠે
 g
 ð
 셤
 ò
 g
 ઠે
 원
 60 PAAGLSAAPVPP-AAAPLLDFSSDSVPPAPRGPLPAAPPTAPERQPSWERSPAASAPSLP 118
 119 PAAAVLPSKLPEDDEPPAR--PPAPAGASPLAEPAAPPSTPAAPKRRGSGSVVVDLLYWR 176
 DIKKTGVVFGASLFLLLSLIVFSIVSVTAYIALALLSVTISFRIYKGVIQAIQKSDEGHP 240
 236
 241 FRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRLFLVDDLVDSLKFAVLMWVFTYVG 300
 237 PRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRLFLVDDLVDSLKFAVLMMVFTYVG 296
 ALFNGLTLILALISLFSIPVIYERHQVQIDHYLGLANKSVKDAMAKIQAKIPGLKRKAD 360
 9
 29
 ĕ
 1 MEDIDQSSLVSSSADSPPRPPPAFKYQFVTEPEDEEDEEDEEDEE-EEEDDEDLEELEVLERK
 PAAGLSAAAVPPAAAAPLLDFSSDSVPPAPRGPLPAAPPAAPERQPSWERSPAAPAPSLP
 121 PAAAVLPSKLPEDDEPPARPPPPPAGASPLAEPAAPPSTPAAPKRRGSGSSVVDLLYWR
 1 MEDIDOSSLVSSSTDSPPRPPAFKYQFVTEPEDEEDEEEEDEEEDBELEELEVLERK
 STRAIN=129/SvcJ7, and 129SvcJ7;
MEDLINE=22376540; PubMed=12488097; DOI=10.1016/S0022-2836(02)01179-8;
 Gaps
 Oertle T., Huber C., van der Putten H., Schwab M.E., Renomic structure and functional characterisation of the promoters
 Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
 4.
 DB 2; Length 356;
 Score 1721.6; DB 2; Lengthered. No. 1.6e-48; Mismatches 7; Indels
 Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AY102281; AAM73503.1; -.
EMBL; AX102286; AAM73508.1; -.
 Van der Putten H.;
Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases
 Interpro, IPR003388; Reficulon.
Pfam; PF02453; Reticulon; 1.
PROSITE; PS50845; RETICULON; 1.
SEQUENCE 356 AA; 38403 MW; 4366C03BA9630B56 CRC64;
 Last sequence update)
Last annotation update)
 GO; GO:0005783; C:endoplasmic reticulum; IDA.
GO; GO:0005515; F:protein binding; IPI.
GO; GO:0001525; P:angiogenesis; IMP.
GO; GO:0007399; P:neurogenesis; IDA.
 Created)
 human and mouse nogo/rtn4.";
J. Mol. Biol. 325:299-323(2003).
 94.4%;
 01-MAR-2003 (TrEMBLrel. 23, 01-MAR-2003 (TrEMBLrel. 23, 05-JUL-2004 (TrEMBLrel. 27,
 STRAIN=129SvcJ7;
Van der Putten H., Mir A.;
 Matches 347; Conservative
PRELIMINARY;
 MGD; MGI:1915835; Rtn4.
 Mus musculus (Mouse).
 Local Similarity
 SEQUENCE FROM N.A.
 SEQUENCE FROM N.A.
 SEQUENCE FROM N.A.
 NCBI_TaxID=10090;
 STRAIN=129/SvcJ7;
Van der Putten H.
 61
 181
 177
 301
 297
 Query Match
Q8BH78
 Q8BH78
SOR DRR REPRETED BY DESCRIPTION OF THE PROPERTY OF THE PROPERT
 g
 ద
 g
 8
 g
 è
 g
 ઠ
 δ
 ò
 ઠે
```

```
60 PAAGLSAAPVPP-AAAPLLDFSSDSVPPAPRGPLPAAPPTAPERQPSWERSPAASAPSLP 118
 PAAGLSAAAVPPAAAAPLLDFSSDSVPPAPRGPLPAAPPAAPERQPSWERSPAAPAPSLP 120
 PAAAVLPSKLPEDDEPPARPPPPPAGASPLAEPAAPPSTPAAPKRRGSG------ 170
 FRIYKGVIQAIQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRLFLVD 201
 DLVDSLKFAVLMWVFTYVGALFNGLTLLILALISLFSIPVIYERHQVQIDHYLGLANKSV 341
 DLVDSLKFAVLMWVFTYVGALFNGLTLLILALISLFSIPVIYERHQAQIDHYLGLANKSV 356
 59
 STRAIN=129/SvcJ7, and 129SvcJ7;
MEDLINE=22376540; PubMed=12488097; DOI=10.1016/S0022-2836(02)01179-8;
OGertle T., Huber C., van der Putten H., Schwab M.E.;
"Genomic Btructure and functional characterisation of the promoters of
 1 MEDIDQSSLVSSSSADSPPRPPPAFKYQFVTEPEDEEDEEDEEDEE-EEEDDEDLEELEVLERK
 171 -----SSVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTIS
 1 MEDIDQSSLVSSSTDSPPRPPPAFKYQFVTEPEDEEDEEEEEDBEEDDEDLEELEVLERK
 Gape
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 111 = 10090;
 23;
 Query Match

93.9%; Score 1712.7; DB 2; Length 375;
Best Local Similarity 91.6%; Pred. No. 3.6e-48;
Matches 347; Conservative 3; Mismatches 6; Indels 23:
 STRAIN=1298vcJ7;
Van der Putten H., Mir A.;
Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AX102282; AAM73504.1; -.
EMBL; AX102286; AAM73509.1; -.
GO; GO:0005783; C:endoplasmic reticulum; IDA.
GO; GO:0005515; F:protein binding; IPI.
GO; GO:0005515; P:protein binding; IPI.
GO; GO:0007399; P:neurogenesis; IMP.
 Van der Putten H.,
Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases
 PROMITE; PS00845; RETICULON; 1.
PROSITE; PS50845; RETICULON; 1.
SROUENCE 375 AA; 40300 MW; 23D9EB19BE671AE6 CRC64;
 Last sequence update)
Last annotation update)
375 AA
 Created)
 KDAMAKIQAKIPGLKRKAD 360
 human and mouse nogo/rtn4.";
J. Mol. Biol. 325:299-323(2003)
 InterPro; IPR003388; Reticulon.
 (TrEMBLrel. 23, C
(TrEMBLrel. 23, I
(TrEMBLrel. 27, I
 SEQUENCE FROM N.A.
 SEQUENCE FROM N.A.
 SEQUENCE FROM N.A.
 STRAIN=129/SvcJ7
 QBBHF5;
01-MAR-2003
01-MAR-2003
 05-JUL-2004
 Name=Rtn4;
 61
 282
 342
 357
 222
 ò
 g
```

SO DR RELEASE OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY

```
177 AASEPVIPSSAEKIMDLKEQPGNTVSSGQEDFPSVLPETAASLPSLSPLSTVSFKEHGYL 236
 STRAIN=129/SvcJ7, and 129SvcJ7; MEDILIBE-22376-840; PhDMed=1248097; DOI=10.1016/S0022-2836(02)01179-8; OCITIE T., Huber C., van der Putten H., Schwab M.E.; Genomic structure and functional characterisation of the promoters of
 61 PAAGLSAAAVPPAAAAPLLDFSSDSVPPAPRGPLPAAPPAAPERQPSWERSPAAPAPSLP
 60 PAAGLSAAPVPP-AAAPLLDFSSDSVPPAPRGPLPAAPPTAPERQPSWERSPAASAPSLP
 237 GNLSAVASTEGTIEETLNEASRELPERATNPFVNRESAEFSVLEYSEMGSSFNGSPKGES
 297 AMLVENTKEEVIVRSKDKEDLVCSAALHNPQESPATLTKVVKEDGVMSPEKTMDIFNEMK
 1 MEDIDQSSLVSSSTDSPPRPPAFKYQFVTEPEDEEDEEEEDEEEDDEDLEELEVLERK
 357 MSVVAPVREEYADFKPFEQAWEVKDTYEGSRDVLAARANMESKVDKKCFEDSLEQKGHGK
 417 DSESRNENASFPRIPELVKDGSRAYITCDSFSSATESTAANIFPVLEDHTSENKTDEKKI
 177 BERKAQIITEKTSPKTSNPFLVAIHDSEADYVTTDNLSKVTEAVVATMPEGLTPDLVQEA
 Gaps
 6; Indels 810;
 121 PAAAVLPSKLPEDDEPPARPPPPAGASPLAEPAAPPSTPAAPKRGSGS-
 InterPro; IPR003388; Reticulon.
Pfam; PP02453; Reticulon; 1.
PR051TE; PS0645; RETICULON; 1.
SEQUENCE 1162 AA; 126612 MW; 855697FBEE11781F CRC64;
 STRAIN=129SvcJ7;
Van der Putten H., Mir A.;
Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AY102284; AAM73506.1; -.
EMBL; AY102286; AAM73511.1; -.
MGD; MGI:1915835; Rtn4.
 to the EMBL/GenBank/DDBJ databases
 89.8%; Score 1637; DB 2; 29.8%; Pred. No. 1.6e-44; ive 2; Mismatches 6;
 IDA
 GO; GO:0005783; C:endoplasmic reticulum;
GO; GO:0005515; F:protein binding; IPI.
GO; GO:0001525; P:angiogenesis; IMP.
GO; GO:0007399; P:neurogenesis; IDA.
 human and mouse nogo/rtn4.";
J. Mol. Biol. 325:299-323(2003)
 Best Local Similarity 29.8
Matches 348; Conservative
 Submitted (MAY-2002)
 Van der Putten H.;
 SEQUENCE FROM N.A.
 SEQUENCE FROM N.A.
 SEQUENCE FROM N.A
NCBI_TaxID=10090;
 STRAIN=129/SvcJ7
 172
 172
 g
 g
 셤
 셤
 셤
 g
 ò
 셤
 à
 8
 ò
 ò
 ò
 ઠે
 120
 118
 239
 236
 299
 296
 359
 PAAAVLPSKLPEDDEPPARPPPPPPAGASPLAEPAAPPSTPAAPKRGGGSSVVDLLYWR 180
 176
 297 GALFNGLTLLILALISLFSIPVIYERHQAQIDHYLGLANKSVKDAMAKIQAKIPGLKRKA 356
 9
 59
 1 MEDIDQSSLVSSSADSPPRPPAFKYQFVTEPEDEEDEEDEE-EEEDDEDLEELEVLERK
 PFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRLFLVDDLVDSLKFAVLMWVFTYV
 PAAGLSAAAVPPAAAAPLLDFSSDSVPPAPRGPLPAAPPAAPERQPSWERSPAAPAPSLP
 PAAGLSAAPVPP-AAAPLIDFSSDSVPPAPRGPLPAAPPTAPERQPSWERSPAASAPSLP
 DIKKTGVV-FGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQAIQKSDEGH
 DIKKTGVVYFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQAIQKSDEGH
 GALFNGLTLLILALISLFSIPVIYERHQVQIDHYLGLANKSVKDAMAKIQAKIPGLKRKA
 1 MEDIDQSSLVSSSTDSPPRPPPAFKYQFVTEPEDEEDEEEEBDEEDDEDLEELEVLERK
 PAAAVLPSKLPEDDEPPAR -- PPAPAGASPLAEPAAPPSTPAAPKRRGSGSVVVDLLYWR
 PFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRLFLVDDLVDSLKFAVLMWVFTYV
 Gaps
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. NCBI_TaxID=10090;
 Mus musculus (Mouse).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
 ر.
د
 DB 2; Length 357;
 Score 1711.5; DB 2; Length
Pred. No. 3.5e-48;
2; Mismatches 7; Indels
 Jin W., Li R., Long M., Shen J., Ju G.;
Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
EMBL, AV114153; AAM77069.1; -.
GO; MGI:191583; ART4.
GO; GO:0005783; C:endoplasmic reticulum; IEA.
InterPro; IPR003388; Reticulon.
Pfam; PF02453; Reticulon; 1.
PROSITE; PSS0845; Reticulon; 1.
SEQUENCE 357 AA; 38566 MW; 73BB3D17DFDBDF15 CRC64;
 Last sequence update)
Last annotation update)
 Last sequence update)
Last annotation update)
 AA
 PRT; 1162 AA
 357
 Created)
 Created)
 Query Match
Best Local Similarity 96.1%;
Matches 347; Conservative 5
 (TrEMBLrel. 22, (TrEMBLrel. 22, (TrEMBLrel. 26, 1
 23,
23,
27,
 (TrEMBLrel. 2 (TrEMBLrel. 2 (TrEMBLrel. 2
 PRELIMINARY;
 PRELIMINARY;
 FROM N.A.
 SEQUENCE FROM N
STRAIN=BALB/c;
 E 357
 D 360
 01-OCT-2002
01-MAR-2004
 01-MAR-2003
01-MAR-2003
 05-JUL-2004
 01-OCT-2002
 Name=Rtn4;
 Name=Rtn4
 360
 09
 119
 237
 357
 61
 121
 240
 300
 181
 177
 Q8K3G7
 OBBGM9
 Q8K3G7
 Q8BGM9
 RESULT 5
08BGM9
1D 08BG
AC 08BG
DT 01-M
DT 05-U
DE RTN4
GN Muse
OC EUKa
```

g

d ò 셤

ð

요

à

셤

à

유

δ

셤

ò

118 171

59

171

| PLNSLLPSTGASVAQPSASPLEVPSPVSYDGIKLEPENPPPYEEAMSVALKTSDSKEEIK 656                                                                                           | 음 <b>강</b> | 1 MEDIDQSSLVSSSADSPPRPPPAFKYQFYTEPEDEEDEEDEEDEEDEEDEEDEEDEEDEELEKKE 59 61 PAAGLSAAAVPPAAAPLLDPSSDSVPPAPRGPLPAAPPAAPRQPSWERSPAAPRSLP 120 |
|------------------------------------------------------------------------------------------------------------------------------------------------------------|------------|-----------------------------------------------------------------------------------------------------------------------------------------|
| PDRGRNAAARBABADVICIACHIIVEMVICHBEGBEGNVCBIAVEBVGUDDUCEIUHDC 216                                                                                            | q ¿        | 60 PAAGLSAVPVPP-AAAPLLDFSSDSVPPAPRGPLPAAPPTAPERQPSWERSPAASAPSLP 118                                                                     |
| 17                                                                                                                                                         | <b>አ</b> ብ | PAAAVLPSKLPEDDEFPARPPAPAGASPLAEPAAPPSTPAAPKRGSGSVDETLFALP                                                                               |
| SPESSEPVDLFSDDSIPEVPQTQEEAVMLMKESLTEVSETVTQHKHKERLSASPQEVGKPY 776                                                                                          | ò          | 172 171                                                                                                                                 |
| 171                                                                                                                                                        | අු         | 177 AASEPVIPSSAEKIMDLKEQPGNTVSSGQEDFPSVLFETAASLPSLSPLSTVSFKEHGYL 236                                                                    |
| LESFOPNLHITKDAASNEIPTLTKKETISLOMEEFNTAIYSNDDLLSSKEDKMKESETFS 836                                                                                           | Š          | 172 171                                                                                                                                 |
| !                                                                                                                                                          | <u>a</u>   | GNLSAVASTEGTIEETLNEASRELPERATNPFVNRESAEFSVLEYSEMGSSFNGSPKGES                                                                            |
| ×                                                                                                                                                          | ờ t        | 172 171                                                                                                                                 |
| SSVSKVPLLLPNVSALESQIEMGNIVKPKVLTKEAEEKLPSDTE                                                                                                               | 8 &        | Prilayent reby vy vkokolokolokolokulani vyborkatili kvy keloky noseloki je v kaloky noseloky noseloky o 17                              |
| SVVDLLYWRDIKKTGVVFGASLFLLISLTVFSIVSVTAYIALA 214                                                                                                            | a<br>a     | 357 MSVVAPVREEYADFKPFEQAWEVKDTYEGSRDVLAARANMESKVDKKCFEDSLEQKSHGK 416                                                                    |
| KEDRSLTAVLSAELNKTSVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALA 1016                                                                                          | ò          | 172 171                                                                                                                                 |
| LLSVTISFRIVKGVIQAIQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKEL 274                                                                                           | qa         | 417 DSESRNENASFPSTPELVKDGSRAYITCDSFTSATESTAANIFPVLEDHTSENKTDEKKI 476                                                                    |
|                                                                                                                                                            | ò          | 172                                                                                                                                     |
| RRLFLVDDLVDSLKFAVLMMVFTYVGALFNGLTLLILALISLFSIPVIYERHQVQIDHYL 334  1                                                                                        | a è        | 477 EERKAQIITEKTSPKTSNPFLVAIHDSEADYVTTDNLSKVTEAVVATMPEGLTPDLVQEA 536                                                                    |
|                                                                                                                                                            | ; A        | -<br>7 CESELNEATGTKIAYETKVDLVQTSEAIQESIYPTAQLCPSFEEAEATPSPVLPDIVMEA                                                                     |
|                                                                                                                                                            | ò          | 172 171                                                                                                                                 |
|                                                                                                                                                            | eg<br>G    | 597 PLNSLLPSTGASVAQPSASPLEVPSPVSYDGIKLEPENPPPYEEAMSVALKTSDAKEEIK 656                                                                    |
|                                                                                                                                                            | ò          | 172 171                                                                                                                                 |
|                                                                                                                                                            | q          | 657 EPESFNAAAQEAEAPYISIACDLIKETKLSTEPSPGFSNYSEIAKFEKSVPDHCELVDDS 716                                                                    |
| (IIEMBLrel. 22, Created) (TIEMBLrel. 22, Last sequence update)                                                                                             | È          | 172 171                                                                                                                                 |
|                                                                                                                                                            | 셤          | 717 SPESEPVDLFSDDSIPEVPQTQEEAVMLMKESLTEVSETVTQHKHKERLSASPQEVGKPY 776                                                                    |
| vanicentur;<br>Mus musculus (Mouse).<br>Britannota, Motanoa, Chondata, Craniata, Vortahvata, Britaloostomi.                                                | ò          | 172 171                                                                                                                                 |
| bunalycia, metazoa, chotaca, crantaca, vercebaca, bucesoscomi,<br>Mammaloris, Butheria, Rodentia, Sciurognathi, Muridae; Murinae, Mus.<br>Mort mastrandon. | qq         | 777 LESFQPNLHITKDAASNEIPTLTKKETISLQMEBFNTAIYSNDDLLSSKEDKMKESETFS 836                                                                    |
| NCBI INALDEIVOUCE<br>(1)                                                                                                                                   | È          | 172 171                                                                                                                                 |
| FROM N.A.                                                                                                                                                  | q          | 837 DSSPIBIIDEFPTFVSAKDDSPKEYTDLEVSNKSEIANVQSGANSLPCSELPCDLSFKNT 896                                                                    |
| Jin W., Long M., Li R., Ju G.;<br>Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.                                                                 | ò          | 172 171                                                                                                                                 |
| AAM77068.1;<br>5; Rtn4.                                                                                                                                    | 셤          | 897 YPKDEAHVSDEFSKSRSSVSKVPLLLPNVSALESQIEMGNIVKPKVLTKEAEEKLPSDTE 956                                                                    |
| C:endoplasmic reticulum; IEA.<br>3388; Reticulon.                                                                                                          | , <b>ở</b> | 172SVVDLLYWRDIKKTGVV-FGASLFLLLSLTVFSIVSVTAYIAL 213                                                                                      |
| į                                                                                                                                                          | ପ୍ର        | 957 KEDRSLTAVLSAELNKTSVVDLLYWRDIKKTGVVYFGASLFLLLSLTVFSIVSVTAYIAL 1016                                                                   |
| MW; 0657502/9441/6A4 CKC04;                                                                                                                                | ò          | 214 ALLSVTISFRIYKGVIQAIQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKE 273                                                                    |
| n 1163;                                                                                                                                                    | q          | 1017 ALLSVTISFRIYKGVIQAIQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKE 1076                                                                  |
|                                                                                                                                                            | ò          | 274 LRRIFLVDDLVDSLKFAVLMMVPTVVGALFNGLTLLILALISLFSIPVIYBRHOVOIDHY 333                                                                    |

ဖ

```
SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
 RGS-----
 Homo sapiens (Human)
 NCBI_TaxID=9606;
 61
 Н
 167
 RESULT 8
RIN4 HUMAN
 ACCOORDING TO THE SECTION OF THE SEC
 q
 셤
 셤
 셤
 g
 ð
 ð
 ద
 ð
 à
 ð
 8
 Straubberg R.L., Feingold E.A., Grouse L.H., Dorge J.G.,

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Hopkins R.F., Jordan H., Moore T., Max S.I., Wubin G.M., Haleh F.,

Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheez T.E.,

Robert S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Robak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Nilalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,

Rahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

Krywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,

Jones S.J., Marra M.A.;

Rand Golf M. Schill All All S., Consellon S., Consellon J.E.,

T. Generation and Initial analysis of more than 15,000 full-length human and mouse CDNA sequences.
9
 SEQUENCE FROM N.A. MEDLINE=22376540; PubMed=12488097; DOI=10.1016/S0022-2836(02)01179-8; Oertle T., Huber C., van der Putten H., Schwab M.E.; "Genomic structure and functional characterisation of the promoters of
 Gaps
 Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
 36;
 MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 87.7%; Score 1598.4; DB 2; Length 392;
82.7%; Pred. No. 2.2e-44;
ive 12; Mismatches 20; Indels 36;
 Strausberg R.;
Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
 SEQUENCE FROM N.A.
Van der Putten H.;
Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
 EMBL; AY102285; AAM64242.1; -.
GO; GO:0005783; C:endoplasmic reticulum; IEA.
InterPro; IPR003388; Reticulon.
Pfam; PF02453; Reticulon; 1.
PROSITE; PS50845; RETICULON; 1.
SEQUENCE 392 AA; 42274 MW; D7B2AA5E839E58AD CRC64;
 01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
Reticulon 4, isoform D (RTM4 isoform B2).
 Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 392 AA
 LGLANKSVKDAMAKIQAKIPGLKRKAD 360
 human and mouse nogo/rtn4.";
J. Mol. Biol. 325:299-323(2003)
 EMBL; BC016165; AAH16165.1; -.
EMBL; AY102278; AAM64247.1; -.
 Best Local Similarity 82.73
Matches 326; Conservative
 PRELIMINARY;
 Similarity
 FROM N.A.
 SEQUENCE FROM N.A.
 TISSUE=Kidney;
 1137
 1077
 334
 SEQUENCE
 Query Match
 096B16
 RESULT 7
Q96B16
 HIDD THE STANDARD OF THE STAND
 음
 셤
 ò
```

```
166
 238
 326
 358
60
 28
 299 VNCTIKELRRLFLYVDDLVDSLKFAVLMMVFTYVGALFNGLTLLILALISLFSVPVIYERH
 PAAGLSAAAVP--PAAAAPLLDFSSDSVPPAPRGPLPAAPPAAPERQPSWERSPAA---P
 207 VTAYIALALLSVTISFRIYKGVIQAIQKSDEGHPFRAYLESEVAISEELVQKYSNSALGH
 239 VTAYIALALLSVTISFRIYKGVIQAIQKSDEGHPFRAYLESEVAISEELVQKYSNSALGH
 267 VNSTIKELRRLFLVDDLVDSLKFAVLMWVFTYVGALFNGLTLLILALISLFSIPVIYERH
 MEDIDOSSLVSSSTDSPPRPPPAFKYQFVTEPEDEEDEEBEEBEEDDEDLEELEVLERK
 116 APSLPPAAAVLPSKLPEDDEPPARPPPPPAGASPLAE------PAAPPSTPAAPKR
 -----GSSVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVS
 SEQUENCE FROM N.A. (ISOFORM 4).
Jin W.-L., Ju G.;
Developmentally-regulated alternative splicing in a novel Nogo-A.";
Submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases.
 SEQUENCE FROM N.A. (ISOFORMS 1; 2 AND 3).
MEDLINE=20129242; PubMed=10667780; DOI=10.1038/35000287;
Prinjha R., Moore S.E., Vinson M., Blake S., Morrow R., Christie G., Michalovich D., Simmons D.L., Walsh F.S.;
"Inhibitor of neurite outgrowth in humans.";
Nature 403:383-384(2000).
 MEDLINE=21010696; PubMed=11126360; DOI=10.1038/sj.onc.1203948; Tagami S., Eguchi Y., Kinoshita M., Takeda M., Tsujimoto Y.; Ah novel protein, RTN-XS, interacts with both Bcl-XL and Bcl-2 on endoplasmic reticulum and reduces their anti-apoptotic activity."; Oncogene 19:5736-5746(2000).
 28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
25-OCT-2004 (Rel. 45, Last annotation update)
Reticulon 4 (Neurite outgrowth inhibitor) (Nogo protein) (Foocen)
(Neuroendocrine-specific protein) (NSP) (Neuroendocrine specific protein C homolog) (RTN-x) (Reticulon 5) (My043 protein).
 Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
 RTN4 HUMAN STANDARD; .PRT; 1192 AÅ.
Q9NQG3; 094962; Q9BXG5; Q9H212; Q9H313; Q9UQ42; Q9Y293; Q9Y2Y7;
Q9Y5UG;
 Yang J., Yu L., Bi A.D., Zhao S.-Y.;
"Assignment of the human reticulon 4 gene (RTN4) to chromosome 2p14-->2p13 by radiation hybrid mapping.";
Cytogenet. Cell Genet. 88:101-102(2000).
 327 QVQIDHYLGLANKSVKDAMAKIQAKIPGLKRKAD 360
 359 QAQIDHYLGLANKNVKDAMAKIQAKIPGLKRKAE 392
 SEQUENCE FROM N.A. (ISOFORMS 1; 2 AND 3).
MEDLINE=20237542; PubMed=10773680;
```

```
TISSUE-Brain, Ovary, Pancreas, Placenta, and Skeletal muscle;
TISSUE-Brain, Ovary, Pancreas, Placenta, and Skeletal muscle;
TISSUE-Brain, Ovary, Pancreas, Placenta, and Skeletal muscle;
A Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
A Strausberg R.D., Colling F.S., Wagner L., Shenmen C.M., Schuler G.D.,
A Alschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhata N.K.,
A Distchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
A Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Usdin T.B., Tochhyuki S., Carninci P., Prange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Brownstein M.J., Wekernan K.J., Matek J.A., Gunarate P.H.,
Roask S.A., McEwan P.J., McKernan R.J., Matek J.A., Gunarate P.H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Pahey J., Helton B., Ketteman M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
C. Mancheller M., Schehl J.E., Jones S.J.M., Marra M.A.,
 TISSUE-Umbilical cord blood;
MBDLINE=20499367; PubMed=11042152; DOI=10.1101/gr.140200;
Zhang Q.-H., Ye M., Wu X.-Y., Ren S.-X., Zhao M., Zhao C.-J., Fu G.,
Shen Y., Fan H.-Y., Lu G., Zhong M., Xu X.-R., Han Z.-G., Zhang J.-W.,
Tao J., Huang Q.-H., Zhou J., Hu G.-X., Gu J., Chen S.-J., Chen Z.;
"Cloning and functional analysis of cDNAs with open reading frames for atomy previously undefined genes expressed in CD34+ hematopoletic stem/progenitor cells."
 MEDLINE=99156230; PubMed=10048485;
Nagase T., Ishikawa K.-I., Suyama M., Kikuno R., Hirosawa M.,
Miyajima N., Tanaka A., Kotani H., Nomura N., Ohara O.;
Miyajima N. the coding sequences of unidentified human genes. XII.
The complete sequences of 100 new cDNA clones from brain which code
for large proteins in vitro.";
 TISSUE=Pituitary; Shou J., Huang Q., Dai M., Mao Y.M., Yu Y., Xu X., Song H., Peng Y., Zhou J., Huang Q., Dai M., Mao Y.M., Yu Y., Xu X., Luo B., Hu K., Chen J., Pepecific protein C (NSP) homolog gene."; Human neuroendocrine-specific protein C (NSP) databases.
 SEQUENCE FROM N.A. (ISOFORM 3).
Gu J.R., Wan 'D.F., Zhao X.T., Zhou X.M., Jiang H.Q., Zhang P.P.,
Qin W.X., Huang Y., Qiu X.K., Qian L.F., He L.P., Li H.N., Yu Y.,
 human cDNA clones with function of inhibiting cancer cell
 TISSUE=Placenta, and Skeletal muscle;
Ito T., Schwartz S.M.;
"Cloning of a member of the reticulon gene family in human.";
Submitted (FEB-1999) to the EMBL/GenBank/DDBJ databases.
 "Isolation of a cell death-inducing gene.";
Submitted (JUN-1998) to the EMBL/GenBank/DDBJ databases.
 Submitted (AUG-1999) to the EMBL/GenBank/DDBJ databases.
 and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
[5]
SEQUENCE FROM N.A. (ISOFORMS 2 AND 3)
 SEQUENCE FROM N.A. (ISOFORM 3).
 SEQUENCE FROM N.A. (ISOFORM 2).
 SEQUENCE FROM N.A. (ISOFORM 3).
 SEQUENCE FROM N.A. (ISOFORM 1).
 Genome Res. 10:1546-1560(2000).
 Res. 5:355-364 (1998).
 TISSUE=Fibroblast;
 Yu J., Han L.H.; "Novel human cDN
 TISSUE=Brain
 Yutsudo M.;
 and mouse
SELECTION OF THE CONTROLL OF THE CONTROLL OF THE CONTROLL OF THE CONTROLL OF THE CONTROLL OF THE CONTROLL OF T
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb.ch).
 The regularization...;

1. To regularization...;

2. Neurosci. Res. 67:559-565 (2002).

2. Indicate the regeneration of the nervous central system in adults.

2. Education of the nervous central system in adults.

2. Isoform 2 reduces the anti-apoptoric activity of Bcl-xl and Bcl-2.

2. This is likely consecutive to their change in subcellular location, from the mitochondria to the endoplasmic reticulum, after binding and sequestration.

2. SUBUNIT: Binds to RTNAR. Interacts with Bcl-xl and Bcl-2.

3. SUBCEILULAR LOCATION: Integral membrane protein. Endoplasmic reticulum Anchored to the membrane domains.

3. SUBCEILULAR LOCATION: Integral membrane domains.

4. ALTERNATIVE PRODUCTS:

5. SUBCEILULAR LOCATION: Subscription of the endoplasmic reticulum through 2 putative transmembrane domains.

6. Isold=QBNQC3-1; Sequence=Displayed;

8. Name=1; Synonyms=RTN 4A, Nogo-B, RTN-XI;

1 Isold=QBNQC3-1; Sequence=USP 005655;

8. Name=2; Synonyms=RTN 4C, Nogo-C, Poocen-S;

1 Isold=QBNQC3-2; Sequence=VSP 005655; VSP_005653;

8. Name=3; Synonyms=RTN 4C, Nogo-C, Poocen-S;

1 Isold=QBNQC3-3; Sequence=VSP_005652, VSP_005653;
 Isold-Q9NQC3-4; Sequence=VSP_005654;
ISOSUB SPECIFICITY: Isoform 1 is specifically expressed in brain
and testis and weakly in heart and skeletal muscle. Isoform 2 is
widely expressed excepted for the liver. Isoform 3 is expressed in
brain, skeletal muscle and adipocytes. Isoform 4 is testis-
 MEDLINE=21069055; PubMed=11201742; DOI=10.1038/35053072;
Fournier A.E., Grandpre T., Strittmatter S.M.;
"Identification of a receptor mediating Nogo-66 inhibition of axonal
 GrandPre T., Nakamura F., Vartanian T., Strittmatter S.M., "Identification of the Nogo inhibitor of axon regeneration as a
 MEDLINE=21888956; PubMed=11891768; DOI=10.1002/jnr.10134; Ng C.E.L., Tang B.L.; "Nogos and the Nogo-66 receptor: factors inhibiting CNS neuron
 SPECIAL STATES Contains 1 reticulon domain. CAUTION: Ref.11 sequence differs from that shown due to frameshifts in positions 1149 and 1156.
 MEDLINE=20129259; PubMed=10667797; DOI=10.1038/35000226;
 Mao Y.M., Xie Y., Zheng Z.H.;
Submitted (MAY-1998) to the EMBL/GenBank/DDBJ databases.
 Sha J.H., Zhou Z.M., Li J.M.;
Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.
SEQUENCE OF 482-1192 FROM N.A. (ISOFORM 1/4).
 SEQUENCE OF 186-1192 FROM N.A. (ISOFORM 1)
 CAB99249.1; -. CAB99250.1; -. BAB18927.1; -.
 EMBL; AJ251383; CAB99248.1; -.
 Nature 403:439-444 (2000).
 Nature 409:341-346(2001)
 Reticulon protein.";
 AJ251385;
AB040462;
 AJ251384;
 regeneration.";
 regeneration.";
 (SSUE=Testis;
 TISSUE=Brain;
 TISSUE=Brain;
 TISSUE=Brain;
 FUNCTION
 REVIEW
 EMBL;
EMBL;
 EMBL;
```

| 71                                                                                                                                                                                                                                                                                                                                                     | QY         187 VVFGASLFLLISLIYFSINSVTAYIALALISVTISFRIXKGVIQAIQKSDEGHPFRAYLE 246           Db         1019 VVFGASLFLLISLIYFSINSVTAYLALLSVTISFRIXKGVIQAIQKSDEGHPFRAYLE 1078           QY         247 SEVAISEBLVQKYSNSALGHYNSTIKELRRLFLVDDLVDSLKFAVLMWVFTYVGALFNGL 306           Db         1079 SEVAISEBLVQKYSNSALGHYNSTIKELRRLFLVDDLVDSLKFAVLMWVFTYVGALFNGL 1138           QY         307 TLLILALISLFSIPVIYERHQVQIDHYLGLANKSVKDAMAKIQAKIPGLKRKAD 360           HIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII | RESULT 9  QGIPNO  ID QGIPNO  AC QGIPNO  DT 05-UUL-2004 (TrEMBLrel. 27, Created)  DT 05-UUL-2004 (TrEMBLrel. 27, Last sequence update)  DT 05-UUL-2004 (TrEMBLrel. 27, Last sequence update)  DT 05-UUL-2004 (TrEMBLrel. 27, Last annotation update)  DR Name=RTN4;  OS Homo sapiens (Human)  OC Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi;  OC Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.  OX NCBI_TaxID=9606; | RN [1] RP SEQUENCE FROM N.A.  RC TISSUE=Bye; RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899; RX Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D., RA Altschul S.F., Zeeberg B., Buetcow K.H., Schaefer C.F., Bhat N.K., RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., RA Brownstein M.J., Ugdin T.B., TOShivuki S., Carninci P., Prange C., | RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., RRebards S., McBeards P.H., Greaten F.J., Malek J.A., Gunaratne P.H., RA Bosak S.A., McBwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., RA Richards S., Morley K.C., Hale S., García A.M., Gay L.J., Hulyk S.W., RA Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A., RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., RA Rodrigues A.C., Grimwood J., Schmutz J., Myers R.M., Butterfeild Y.S., D. Myers R.M., Butterfield Y.S., D. Myers R.M., Butterfield Y.S., D. Myers R.M., Butterfield Y.S., D. Mershand M. Schmutz J., Myers R.M., Butterfield Y.S., D. Mershand M. Schmutz J., Myers R.M., Butterfield Y.S., D. Mershand M. Schmutz J., Myers R.M., Butterfield Y.S., D. Myers R.M., Butterfield Y.S., D. Mershand M. Schmutz J., Myers R.M., Butterfield Y.S., D. Mershand M. Schmutz J., Myers R.M., Butterfield Y.S., D. Mershand M. Schmutz J., Myers R.M., Butterfield Y.S., D. Mershand M. Schmutz J., Myers R.M., Butterfield Y.S., D. Mershand M. Schmutz J., Myers R.M., Butterfield Y.S., D. Mershand M. Schmutz J. Myers R.M., Butterfield Y.S., D. Mershand M. Schmutz J. Myers R.M., Butterfield Y.S., D. Mershand M. Schmutz J. Myers R.M., Butterfield Y.S., D. Mershand M. Schmutz J. Myers R.M., Butterfield Y.S., D. Mershand M. Schmutz J. Myers R.M., Butterfield Y.S., D. Mershand M. Schmutz J. Myers R.M., Butterfield Y.S., D. Mershand M. Schmutz J. Myers R.M., Butterfield Y.S., D. Mershand M. Schmutz J. Myers R.M., Butterfield Y.S., D. Mershand M. Schmutz J. Myers R.M., Butterfield Y.S., D. Mershand M. Schmutz J. Myers R.M., Butterfield Y.S., D. Myers R.M. Butterfield Y.S., D. Mershand M. Schmutz J. Myers R.M. Butterfield Y.S., D. Myers R.M. Butterfield Y.S., D. Mershand M. Schmutz J. Myers R.M. Butterfield Y.S., D. Matterfield Y.S., D. Mershand M. Schmutz J. Myers R.M. Butterfield Y.S., D. Mershand M. S. Mershand M. S. Matterfield Y. M. Schmutz J. Mershand M. M. Schmutz J. | RA JORGE S.J., Marra M.A.;  RA JORGE S.J., Marra M.A.;  RT "Generation and initial analysis of more than 15,000 full-length human man mouse cDNA sequences.";  RT and mouse cDNA sequences.";  RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  RN [20]  RN SEQUENCE FROM N.A.  RA Strausberg R.;  RA Strausberg R.;  RA Strausberg R.;  RA Strausberg R.;  RD SEMEL, ECO71848; AAH71848.1;  DR EMBL; ECO71848; AAH71848.1;  DR GO; CO:0005783; C:endoplasmic reticulum; IEA. |
|--------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|-----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|-------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|--------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|--------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| EMBL; AB040463; BAB18928.1; EMBL; AF148537; AAG12176.1; EMBL; AF148538; AAG12177.1; EMBL; AF087901; AAG12205.1; EMBL; AF32099; AAG40878.1; EMBL; AF322047; AAD31021.1; EMBL; AF323048; AAD31022.1; EMBL; AF323048; AAD31022.1; EMBL; AF332048; AAD3702.1; EMBL; AB015639; BAA83712.1; EMBL; AB020693; BAA74909.2; ALT_INIT. EMBL; BC001035; AAH0109.1; | Match   83.3%; Score 1518.4; DB 1; Length 1192;                                                                                                                                                                                                                                                                                                                                                                                                                                                     | APSLPPAAAVLPSKLPEDDEPPARPPPPAGASPLAEPAAPPSTPAAPKR                                                                                                                                                                                                                                                                                                                                                                                                     | 299 EMGSSFSVSPKAESAVIVANPREEIIVKNKDEEEKLVSNNILHNQQELPTALTKLVKEDE 358 171                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   | 171                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            | SPEESEATPSPVLPDIVMEAPLNSAVPSAGASVIQPSSSPLEASSVNYESIKHEPENPPP YEEAMSVSLKKVSGIKEEIKEPENINAALQETEAPYISIACDLIKETKLSAEPAPDFSDY SEMAKVEQPVPDHSELVEDSSPDSEPVDLFSDDSIPDVPQKQDETVMLVKESLTETSFES                                                                                                                                                                                                                                                                                               |

g &

S

```
PROSITE; PS50845; RETICULON; 1. SEQUENCE 986 AA; 108449 MW;
 KAD 360
 KAE 986
 RPPP-
 m
 73
 86
 106
 139
 168
 178
 238
 864
 358
 88
 47
 21
 132
 168
 168
 172
 984
 Query Match
 RESULT 11
 SOR
 ઠ
 셤
 ò
 셤
 ò
 셤
 ò
 셤
 ò
 셤
 à
 셤
 ઠે
 g
 ò
 셤
 ઠે
 셤
 ઠે
 유
 ò
 g
 ò
 셤
 ò
 원
 ò
 셤
 ઠે
 셤
 ò
 d
 4
 198
 318
 GPLPAAPPAAPERQPSWERSPAA---PAPSLPPAAAVLPSKLPEDDEPPARPPPPAGA 148
 62 GPLPAAPPVAPERQPSWDPSPVSSTVPAPSPLSAAAVSPSKI.PEDDEPPARPPPPPPASV 121
 181
 258
 241
 242 YSNSALGHVNCTIKELRRLFLVDDLVDSLKFAVLMMVFTYVGALFNGLTLLILALISLFS 301
 91
 61
 01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
RNT4 (RTN4 isoform Ab) (RTN4 isoform D) (RTN4 isoform B)
 Oertle T., Huber C., van der Putten H., Schwab M.E.; "Genomic structure and functional characterisation of the promoters of human and mouse nogo/rtn4": J. Mol. Biol. 325:299-323(2003).
 122 SPQAEPVWTPPAPAPPSTPAAPKRGSSGSVVVDLLYWRDIKKTGVVFGASLFLLLS
 SPLAE------PAAPPSTPAAPKRRG-SGSSVVDLLYWRDIKKTGVVFGASLFLLLS
 LTVFSIVSVTAYIALALLSVTISFRIYKGVIQAIQKSDEGHPFRAYLESEVAISEELVQK
 YSNSALGHVNSTIKELRRLFLVDDLVDSLKFAVLMWVFTYVGALFNGLTLLILALISLFS
 34 DEEDEEEEEBBEEEDDEDLEELEVLERKPAAGLSAAAVP--PAAAAPLLDFSSDSVPPAPR
 MEDLINE=22376540; PubMed=12488097; DOI=10.1016/S0022-2836(02)01179-8;
 Gaps
 Eukaryota, Metazoa; Chordata; Craniata, Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 15;
 DB 2; Length 343;
 TISSUE-TEACH (MAY-2002) to the EMBL/GenBank/DDBJ databases.
Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AY102285; AAM64244.1; -.
EMBL; AY123246; AAM64250.1; -.
EMBL; AY123249; AAM64251.1; -.
EMBL; AY123249; AAM64253.1; -.
EMBL; AY123250; AAM64254.1; -.
EMBL; AY123345; AAM64254.1; -.
 17; Indels
 319 IPVIYERHQVQIDHYLGLANKSVKDAMAKIQAKIPGLKRKAD 360
 databases
813207C29AB15BA4 CRC64;
 80.7%; Score 1471.5; DB : 86.8%; Pred. No. 2.3e-40; ive 13; Mismatches 17
 to the EMBL/GenBank/DDBJ
 986
 (RTN4 isoform G) (RTN4 isoform Aa)
 PRT;
36918 MW;
 Query Match
Best Local Similarity 86.84
Matches 297; Conservative
 PRELIMINARY;
 Van der Putten H.;
Submitted (MAY-2002)
 Homo sapiens (Human)
Ą.
 SEQUENCE FROM N.A.
 SEQUENCE FROM N.A.
 SEQUENCE FROM N.A.
 NCBI_TaxID=9606
343
 TISSUE=Testis;
 TISSUE=Testis;
 302
 92
 149
 182
 199
 259
SEQUENCE
 081UA4
 RESULT 10
081UA4
1D 081UA4
DT 001-MA
DT 01-MA
DT 01-MA
DT 01-MA
DT 05-JI
DE RNT4 (2)
RN MED NAME
OX NCBI
RN CON NCBI
RN CON NCBI
RN CON NCBI
RN CON NCBI
RN CON NCBI
RN CON NCBI
RN CON NCBI
RN CON NCBI
RN CON NCBI
RN CON NCBI
RN CON NCBI
RN CON NCBI
RN CON NCBI
RN CON NCBI
RN CON NCBI
RN CON NCBI
RN CON NCBI
RN CON NCBI
RN CON NCBI
RN CON NCBI
RN CON NCBI
RN CON NCBI
RN CON NCBI
RN CON NCBI
RN CON NCBI
RN CON NCBI
RN CON NCBI
RN CON NCBI
RN CON NCBI
RN CON NCBI
RN CON NCBI
RN CON NCBI
RN CON NCBI
RN CON NCBI
RN CON NCBI
RN CON NCBI
RN CON NCBI
RN CON NCBI
RN CON NCBI
RN CON NCBI
RN CON NCBI
RN CON NCBI
RN CON NCBI
RN CON NCBI
RN CON NCBI
RN CON NCBI
RN CON NCBI
RN CON NCBI
RN CON NCBI
RN CON NCBI
RN CON NCBI
RN CON NCBI
RN CON NCBI
RN CON NCBI
RN CON NCBI
RN CON NCBI
RN CON NCBI
RN CON NCBI
RN CON NCBI
RN CON NCBI
RN CON NCBI
RN CON NCBI
RN CON NCBI
RN CON NCBI
RN CON NCBI
RN CON NCBI
RN CON NCBI
RN CON NCBI
RN CON NCBI
RN CON NCBI
RN CON NCBI
RN CON NCBI
RN CON NCBI
RN CON NCBI
RN CON NCBI
RN CON NCBI
RN CON NCBI
RN CON NCBI
RN CON NCBI
RN CON NCBI
RN CON NCBI
RN CON NCBI
RN CON NCBI
RN CON NCBI
RN CON NCBI
RN CON NCBI
RN CON NCBI
RN CON NCBI
RN CON NCBI
RN CON NCBI
RN CON NCBI
RN CON NCBI
RN CON NCBI
RN CON NCBI
RN CON NCBI
RN CON NCBI
RN CON NCBI
RN CON NCBI
RN CON NCBI
RN CON NCBI
RN CON NCBI
RN CON NCBI
RN CON NCBI
RN CON NCBI
RN CON NCBI
RN CON NCBI
RN CON NCBI
RN CON NCBI
RN CON NCBI
RN CON NCBI
RN CON NCBI
RN CON NCBI
RN CON NCBI
RN CON NCBI
RN CON NCBI
RN CON NCBI
RN CON NCBI
RN CON NCBI
RN CON NCBI
RN CON NCBI
RN CON NCBI
RN CON NCBI
RN CON NCBI
RN CON NCBI
RN CON NCBI
RN CON NCBI
RN CON NCBI
RN CON NCBI
RN CON NCBI
RN CON NCBI
RN CON NCBI
RN CON NCBI
RN CON NCBI
RN CON NCBI
RN CON NCBI
RN CON NCBI
RN CON NCBI
RN CON NCBI
RN CON NCBI
RN CON NCBI
RN CON NCBI
RN CON NCBI
RN CON NCBI
RN CON NCBI
RN CON NCBI
RN CON NCBI
RN CON NCBI
RN CON NCBI
RN CON NCBI
RN CON NCBI
RN CON NCBI
RN CON NCBI
RN CON NCBI
RN CON NCBI
RN CON NCBI
RN CON NCBI
RN CON NCBI
RN CON NCBI
RN CON NCBI
RN CON NCBI
RN CON NCBI
RN CON NC
Š
 8
 a
 ઠે
 셤
 ઠે
 a
 g
 ò
 요
 8
 q
 ò
```

```
16;
 144 LTKLVKEDEVVSSEKAKDSFNEKRVAVEAPMREEYADFKPFERVWEVKDSKEDSDMLAAG 203
 263
 443
 138
 167
 167
 167
 171
 743
 803
 YWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQAIQKSDE 237
 863
 297
 923
 323
 131
 444 KHEPENPPPYEEAMSVSLKKVSGIKEEIKEPENINAALQETEAPYISIACDLIKETKLSA 503
 504 EPAPDFSDYSEMAKVEQPVPDHSELVEDSSPDSEPVDLFSDDSIPDVPQKQDETVMLVKE 563
 564 SLTETSFESMIEYENKEKLSALPPEGGKPYLESFKLSLDNTKDTLLPDEVSTLSKKEKIP 623
 624 LQMEELSTAVYSNDDLFISKEAQIRETETFSDSSPIELIDEPPTLISSKTDSFSKLAREY 683
 177 TAMPER 174
 383
 72
 40
 85
 804 YWRDIKKTGVVFGASLFLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQAIQKSDE
 ---EVLERKPAAGLSAAAVPP
 684 TDLEVSHKSEIANAPDGAGSLPCTELPHDLSLKNIQPKVEEKISFSDDFSKNGSATSKVL
 744 LLPPDVSALATQAEIESIVKPKVLVKEAEKKLPSDTEKEDRSPSAIFSAELSKTSVVDLL
 GHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRLFLVDDLVDSLKFAVLMWVFT
 GHPFRAYLESEVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDSLKFAVLMWVFT
 ----AAPLLDFSSDS----
 384 LYPAAQLCPSFEESEATPSPVLPDIVMEAPLNSAVPSAGASVIQPSSSPLEASSVNYESI
 264 AATESIATNIFPLLGDPTSENKTDEKKIEEKKAQIVTEKNTSTKTSNPFLVAAQDSETDY
 324 VITDNLTKVTEEVVANMPEGLTPDLVQEACESELNEVTGTKIAYETKMDLVQTSEVMQES
 ------VPPAPRGPLPAAPBARGO-------VPPAPRGPLPAAPERQ
 ---PPPAGASPLAEPAAPPSTPA------APKRR-----
 Gaps
 549;
 55.5%; Score 1012.1; DB 2; Length 986; 27.7%; Pred. No. 3.3e-24; ive 33; Mismatches 71; Indels 549;
 --EDDEPP-------
OCDE8F647036415A CRC64;
 DIDOSSLVSSSTDSPPRPPAFKYOFVTBPEDE----EDEEE---
 --I.EEL----
 -----PSWERSPAAPAPSLPP----
 -----BSGS-----
 Best Local Similarity 27.7
Matches 250; Conservative
 ----EEDE----

 AA-----
```

```
975 FAVLMMVFTYVGALFNGLTLLILALISLFSIPVIYERHQAQIDHYLGLANKSVKDAMAKI 1034
 8
 168
 974
 107
 ----- 106
 795 SRSSVSKVPLLLPNVSALESQIEMGNIVKPKVLTKEAEEKLPSDTEKEDRSLTAVLSAEL 854
 63
 915 IQAIQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRLFLVDDLVDSLK
 FAVLAMVETYVGALFNGLTLLILALISLFSIPVIYERHQVQIDHYLGLANKSVKDAMAKI
 48 PENPPPYEEAMSVALKTSDAKEEIKEPESFNAAAQEAEAPYISIACDLIKETKLSTEPSP
 615 IPEVPOTOEEAVMLMKESLTEVSETVTOHKHKERLSASPOEVGKPYLESPOPNLHITKDA
 735 VSAKDDSPKEYTDLEVSNKSEIANVQSGANSLPCSELPCDLSFKNTYPKDEAHVSDEFSK
 171
 IQAIQKSDEGHPFRAYLESEVAISEELVOKYSNSALGHVNSTIKELRRLFLVDDLVDSLK
 17 PPRPPP---AFKYQFVTEPEDEEDEEEDDEEDDE------DLEELEVLERKPAA
 675 ASNEIPTLTKKETISLQMEEFNTAIYSNDDLLSSKEDKMKESETFSDSSPIEIIDEFPTF
 171 --SSVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGV
 64 GLS-----AAAVP-----PAAAAPLLDFSSDSVPPAPR-------
 Gaps
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
 54.4%; Score 992.2; DB 2; Length 578;
42.4%; Pred. No. 4.1e-24;
ive 13; Mismatches 79; Indels 225;
 Tozaki H., Hirata T.;
Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AB073672; BAC75974.1; -.
GO; GO:0005783; C:endoplasmic reticulum; IEA.
InterPro; IFR003388; Reticulon.
Pfam; PF02453; Reticulon; 1.
 578 AA; 63696 MW; 832670C171E4AC61 CRC64;
 Last sequence update)
Last annotation update)
 ----GPLPAAPPAAPERQP-
 Created)
 PRT;
 01-JUN-2003 (TrEMBLzel. 24, C)
01-JUN-2003 (TrEMBLzel. 24, Li
01-OCT-2003 (TrEMBLzel. 25, Li
Nago-A (Fragment)
Name=Nogo-A;
Mus musculus (Mouse)
 ||||||||||||
1035 QAKIPGLKRKAE 1046
 349 QAKIPGLKRKAD 360
 Matches 233; Conservative
 PRELIMINARY;
 Similarity
 SEQUENCE FROM N.A.
 169
 NCBI_TaxID=10090;
 157 PPSTP
 92 ----
 Q80W95;
01-JUN-2003
 289
 NON TER
SEOUENCE
 169
 229
 Query Match
Best Local (
 RESULT 12
Q80W95
 g
 ò
 d
 g
 ઠે
 g
 유
 ACCOCCOS ON THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF T
 a
 셤
 à
 8
 ò
 ઠે
 ò
 g
 ò
 ò
 ò
 14;
 256
 316
 374
 105
 142
 554
 ----GASPLAEPA----A 156
 375 KTSNPPLVAIHDSEADYVTTDNLSKVTEAVVATMPEGLTPDLVQEACESELNEATGTKIA 434
 134
 435 YETKVDLVQTSEAIQESIYPTAQLCPSFEEAEATPSPVLPDIVMEAPLNSLLPSTGASVA 494
 PYISIACDLIKETKLSTEPSPEFSNYSEIAKFEKSVPDHCELVDDSSPESEPVDLFSDDS 614
 35
 20
 72
 STRAIN=129/SvcJ7, and 129SvcJ7;
MEDLINE=22376540; PubMed=12488097; DOI=10.1016/S0022-2836(02)01179-8;
Oertle T., Huber C., van der Putten H., Schwab M.E.;
"Genomic structure and functional characterisation of the promoters of
 257 FEQAWEVKDTYEGSRDVLAARANMESKVDKKCFEDSLEQKGHGKDSESRNENASFPRIPE
 : | | | | : | | | 317 LVKDGSRAYITCDSFSSATESTAANIFPVLEDHTSENKTDEKKIEERK--AQIITEKTSP
 -----PSWERSPAAPAPSLP----PAAAVLPSKLPEDD
 495 QPSASPLEVPSPVSYDGIKLEPENPPPYEEAMSVALKTSDSKEEIKEPESFNAAAQEAEA
 DKEDLVCSAALHNPQESPATLTKVVKEDGVMSPEKTMDI FNEMKMSVVAPVREEYADFKP
 ------EELEVLERKPAAGLSAAVPP
 AAAAPLIDFSSDS-------VPPAPRGPLPAAPPAAFERQ-----
 Gaps
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Mus
 55.4%; Score 1010.2; DB 2; Length 1046; 29.2%; Pred. No. 4.3e-24;
 498;
 ------BDEBEEDEEDDED
 80; Indels
 DOSSLVSSSTDSPPRPPPA----FKYQFVTEPEDE------
 1046 AA; 114221 MW; 8CE2E2238ED51222 CRC64;
 STRAIN=129/SvcJ7;
Van der Putten H.;
Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
 Van der Putten H., Mir A.;
Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AX102286; AAM73502.1; --
EMBL; AX102286; AAM73507.1; --
 Last sequence update)
Last annotation update)
 -----PARPPP------
 MGD; MGI:1915835; Rtn4.
GO; GO:0005783; C:endoplasmic reticulum; IDA.
GO; GO:0005515; F:protein binding; IPI.
GO; GO:0001225; F:angiogenesis; IMP.
GO; GO:0007399; P:neurogenesis; IDA.
InterPro; IRRO3388; Reticulon.
PROSITE; PS50845; RETICULON; 1.
 1046 AA
 29.2%; Pred.
 -----PPPA-----
 Created)
 human and mouse nogo/rtn4.";
J. Mol. Biol. 325:299-323 (2003).
 23,
23,
 Best Local Similarity 29.2
Matches 249; Conservative
PRELIMINARY;
 01-MAR-2003 (TrEMBLrel. 05-JUL-2004 (TrEMBLrel.
 (TrEMBLrel.
 Mus musculus (Mouse).
 SEQUENCE FROM N.A.
 SEQUENCE FROM N.A.
 FROM N.A.
 NCBI_TaxID=10090;
 SEQUENCE FROM N. STRAIN=129SvcJ7;
 01-MAR-2003
01-MAR-2003
 Name=Rtn4;
 Ŋ
 36
 21
 73
 555
 SEQUENCE
 106
 135
 Query Match
 143
```

8 6 6 6 6

ð

g

ò

8 S

ò

```
Similarity
 KIPGLKRKAE
 SEQUENCE FROM N.A.
 NCBI_TaxID=9031;
 Name=NOGO
 17
 107
 171
 291
 630
 92
 107
 129
 Query Match
 Local
 Q6RSS8
 Gallus
 RESULT 14
Q6RSS8
 8888888888
 g
 셤
 g
 ò
 g
 ò
 요
 ద
 셤
 g
 ò
 음
 ò
 ð
 ઠ
 ઠે
 ò
 ò
 508
 287
 288 IANVOSGANSLPCSELPCDLSFKNTYPKDEAHVSDEFSKSRSSVFKVPLLLPNVSALESQ 347
 348 IEMGNIVKPKVLTKEAEEKLPSDTEKEDR--------SLTAVLSAELNK 388
 230
 448
 290
 350
 ------KLPEDDEPPARPPPPPAGASPLAEPAPPSTPAAPKRRGSG 170
 AIQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKEIRRLFLVDDLVDSLKFA
 228 NTAIYSNDDLLSSKEDKMKESETFSDSSPIEIIDEFPTFVSAKDDSPKEYTDLEVSNKSE
 -- SWERSPAAPAPSLPPAAAVLPS-
 SSVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQ
 AIQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRLFLVDDLVDSLKFA
 VLMWVFTYVGALFNGLTLLILALISLFSIPVIYERHQVQIDHYLGLANKSVKDAMAKIQA
VSETVTQHKHKERLSASPQEVGKPYLESFQPNLHITKDAASNEI PTLTKKETISLQMEEF
 Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
VCBI_TaxID=10090;
 Strausberg R.;
Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases.
 Created)
Last sequence update)
Last annotation update)
 Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
 639 AA
 SEQUENCE FROM N.A.
STRAIN=FVB/N; TISSUE=Mammary tumor. C3;
 PRT;
 22,
22,
 PRELIMINARY;
 01-OCT-2002 (TrEMBLrel.
01-OCT-2002 (TrEMBLrel.
01-MAR-2004 (TrEMBLrel.
 KIPGLKRKAD 360
 |||||||||||
KIPGLKRKAE 578
 Rtn4 protein.
Name=Rtn4;
 107
 107
 389
 231
 449
 291
 509
 171
 351
 569
 Q8K290;
 Q8K290
유
 8
 g
 8
 g
 ò
 셤
 ò
 g
 엄
 В
 ID
DDTTDDDTTDDDTTDDDTTDDDTTTDD
 8
 ò
 8
```

```
168
 ------KLPEDDEPPARPPPPAGASPLAEPAAPPSTPAAPKRGSG 170
 -----SLTAVLSAELNK 449
 231 AIQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRLFLVDDLVDSLKFA 290
 569
 106
 349 IANVOSCANSLPCSELPCDLSFKNTYPKDEAHVSDEFSKSRSSVSKVPLLLPNVSALEŠO 408
 VLMWVFTYVGALFNGLTLLILALISLFSIPVIYERHQVQIDHYLGLANKSVKDAMAKIQA 350
 629
 289 NTAIYSNDDLLSSKEDKMKESETFSDSSPIEIIDEFPTFVSAKDDSPKEYTDLEVSNKSE 348
 63
 510 AIQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRLFLVDDLVDSLKFA
 SSVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQ
 ----DLEELEVLERKPAA
 109 PENPPPYEEAMSVALKTSDAKEEIKEPESFNAAAQEAEAPYISIACDLIKETKLSTEPSP
 229 VSETVTQHKHKERLSASPQEVGKPYLESFQPNLHITKDAASNEIPTLTKKETISLQMEEF
 ----SWERSPAAPABLPPAAAVLPS-
 Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Archosauria, Aves, Neognathae, Galliformes, Phasianidae, Phasianinae,
 Gaps
 Caltharp S.A., Pira C.U., McNeill D.S., Liwnicz B.H., Oberg K.C.; Submitted (DEC-2003) to the EMBL/GenBank/DDBJ databases.
EMBL, AY494005; AAS18427.1; -- GO; GO:0005783; C:endoplasmic reticulum; IEA.
 Indels 225;
 64 GLS-----AAAVP-----PAAAAPLLDFSSDSVPPAPR-----
 Length 639;
 70312 MW; 309A19DA37603F11 CRC64;
 05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Neurite outgrowth inhibitor NOGO-A (Fragment).
 79;
 DB 2;
 54.2%; Score 988.7; DB 2 42.2%; Pred. No. 6.8e-24;
 PPRPPP---AFKYQFVTEPEDEEDEEEEDEEDDE-
EMBL; BC032192; AAH32192.1; -.
MGD; MGI:191885; REIA.
GO; GO:0005783; C:endoplasmic reticulum; IEA
InterPro; IPR003388; Reticulon.
 658 AA
 409 IEMGNIVKPKVLTKEAEEKLPSDTEKEDR-----
 14; Mismatches
 ---GPLPAAPPAAPERQP
 PRT;
 Pfam; PF02453; Reticulon; 1.
PROSITE; PS50845; RETICULON; 1.
SEQUENCE 639 AA; 70312 MW;
 Matches 232; Conservative
 PRELIMINARY;
 351 KIPGLKRKAD 360
 Gallus gallus (Chicken)
```

```
Gaps 16;
 VLERKPAAGLSAAAVPPAAAAPL----LDFSSD---SVPPAP---RGPLPAAPPAAP 102
 E----ROPSWERSPAAPAPSLP-- 120
 135
 383 LSVRNVEVKTEDDAHALKKSLQAIDREVPEVSMVSLPATGTSPSSTEKEIVSVGKPEAFE 442
 195
 255
 553
 VQKYSNSALGHVNSTIKELRRLFLVDDLVDSLKFAVLMMVFTYVGALFNGLTLLILALIS 315
 92 QLGTFVTTASYENVKKEAEKPPLYQEAVNMPLTQAQEAKEELTLKKADRESSTSPEDLET 151
 152 PYISIACDLIKETKVSGESASPSLTDYSTTPITEHLSQDVSEHKELAEKLSPQFGKCDLF 211
 DDFVMLVDPKTGTEFVAEVTDRETVHKNESKDISNEIRDEKRÖ------APLTELPCD 382
 24
 91
 34
 34
 ----DEDLEELE 55
 -----PAAAVLPSKL-----PEDDE
 DLVQTSESVQETLKPVTQLCPSFEDSEAAPSPVLPDIVMEAPLSSGTAGAEASTVQLETS
 PPARPPPPPAGASPLAEPAAPPSTPAAPKRRGSGSSVVDLLYWRDIKKTGVVFGASLFL
 LLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQAIQKSDEGHPFRAYLESEVAISEEL
 494 LLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQAIQKSDEGHPPRAYLESDVAVSEEL
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
 Indels 305;
 ; Score 960.5; DB 2; Length 658;
; Pred. No. 6.1e-23;
41; Mismatches 70; Indels 305,
 316 LFSIPVIYERHQVQIDHYLGLANKSVKDAMAKIQAKIPGLKRKAD 360
 614 LFSVPVIYERHQAQIDHYLGLVNKNVKDAMAKIQAKIPGLKRKTE 658
 05-JUL-2004 (Rel. 41, Last Sequence update)
Reticulon 4 (Neurite outgrowth inhibitor) (Nogo protein).
Name=Rtn4; Synonyms=NOGO;
Elkarvore...
 72075 MW; 14B7A000C5E8CDA5 CRC64;
 DIDOSS-----LVSSSTDSPPRPPAF----
 35 -----EEDEEE------EEDEEED--
 199 AA.
 -----KYQFV-----
 SEQUENCE FROM N.A.
STRALM-317-L.I. TISSUE=Adipocyte;
Coulson A.C., Craggs P.D., Morris N.J.;
MONUSE VP20/KIN4C CDNA.";
 35 ----
 Pfam; PF02453; Reticulon; 1.
PROSITE; PS50845; RETICULON; 1.
InterPro; IPR003388; Reticulon.
 RTN4 MOUSE STANDARD; E 099P72; Q9CTE3; 28-FEB-2003 (Rel. 41, Created) 28-FEB-2003 (Rel. 41, Last seq.
 52.7%;
 Best Local Similarity 35.59
Matches 229; Conservative
 NON TER 1
SEQUENCE 658 AA;
 NCBI_TaxID=10090;
 32
 331
 256
 e
 25
 212
 26
 103
 121
 136
 196
 Query Match
 S T S R R
 ò
 셤
 요
 ò
 업
 ò
 임
 ð
 g
 ò
 q
 ò
 g
 ò
 g
 ò
 g
 ઠે
 g
 ò
 g
 ò
```

```
RCG STRAIN-C57BL/64; TISSUB=Embryo; RC STRAIN-C57BL/64; TISSUB=Embryo; RC STRAIN-C57BL/64; TISSUB=Embryo; RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S., RA Nikaido I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H., Radacki I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H., Radacki R., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T., Badarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J., Radackenbush J., Batackenbush J., Ranapin A., Matsuda H., Batalov S., Beisel K.W., Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S., Raballa E., Dragani T.A., Fletcher C.F., Fortrest A., Frazer K.S., R. Dalla E., Dragani T.A., Fletcher C.F., Fortrest A., Frazer K.S., R. Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D., R. Anaia A., Kawaji H., Kawasawa Y., Kedalerski R.M., King B.L., A. Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A., Ragolott D.R., Maltais L., Marchionni L., McKenzie L., Miki H., R. Magoshima T., Numata R., Pontius J.U., Oli D., Remachandran S., Petrovsky N., Pillai R., Pontius J.U., Oli D., Ramachandran S., Rangashima T., Numata R., Pontius J., Ring B.Z., Ringwald M., Schnada K., Sandelin A., Schnada K., Sandelin A., Schnada K., Sandelin A., Schnada K., Sandelin A., Churchis A., Yanagisawa M., Yang I., Yang L., Raylawa T., Ronno H., Nakamura M., Sakazume N., Sato K., Rilara A., Hashikawa T., Konno H., Nakamura M., Sakazume N., Sato K., Rilara A., Hashikawa T., Konno H., Nakawura K., Arakawa T., Pukuda S., R. Hara A., Hashikawa T., Konno H., Nakawura K., Shinagawa T., Rhara A., Hashikawa T., Konno H., Nakawura K., Shinagawa T., Rhara A., Hashikawi Y., Sakai K., Shinagawa T., Rhara A., Hashikawi Y., Rhara A., Hashikawi Y., Rhara K., Shinagawa T., Rhara A., Hashikawi Y., Rhara K., Shinagawa T., Rhara A., Hashikawi Y., Rhara K., Shinagawa T., Rhara A., Hara A., Hara A., Hara K., Shinagawa T., Rhara A., Hara A., Hara K., Rhara K., Shinagawa T., Rhara Y., Hara
 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce) or send an email to license@isb-sib.ch).
 Birney E., Hayashizaki Y.; "Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs."; Nature 420:563-573(2002).
 FUNCTION: Potent neurite outgrowth inhibitor which may also help block the regeneration of the nervous central system in adults (By
 similarity).
SUBCELLULAR LOCATION: Integral membrane protein. Anchored to the
membrane of the endoplasmic reticulum through 2 putative
 EMBL; AKO03859; AMNOTATED_CDS.

EMBL; AKO03859; -; NOT ANNOTATED_CDS.

MGD; MGI:1915835; Rtn4-

MGD; MGI:1915835; Rtn4-

MGD; MGI:1915835; Rtn4-

GO; GO:0005783; C:endoplasmic reticulum membrane; ISS.

GO; GO:0005515; C:integral to endoplasmic reticulum membrane; ISS.

GO; GO:0005515; P:protein binding; ISS.

GO; GO:001987; P:negative regulation of anti-apoptosis; ISS.

GO; GO:0007399; P:neurogenesis; IDA.
 similarity).
SUBUNIT: Binds to RTM4R. Interacts with Bcl-xl and Bcl-2 (By
 Alternative splicing; Endoplasmic reticulum; Transmembrane.
Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases.
 Cytoplasmic (Potential). Potential.
 Bvent=Alternative splicing; Named isoforms=1;
Comment=A number of isoforms may be produced;
 -!- SIMILARITY: Contains 1 reticulon domain.
 transmembrane domains (By similarity).
 isoId=Q99P72-1; Sequence=Displayed;
 InterPro; IPR003388; Reticulon.
 Pfam; PF02453; Reticulon; 1.
PROSITE; PS50845; RETICULON; 1.
 EMBL; AF326337; AAK08076.1; -.
 SEQUENCE OF 170-199 FROM N.A.
 ALTERNATIVE PRODUCTS:
 TRANSMEM
```

```
133 DDEPPARPPPPAGASPLAEPAAPPSTPAAPKRRGSGSSVVDLLYWRDIKKTGVVFGAS 192
 193 LFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQAIQKSDEGHPFRAYLESEVAIS 252
 EELVQKYSNSALGHVNSTIKELRRLFLVDDLVDSLKFAVLMWVFTYVGALFNGLTLLILA 312
 92 BELVQKYSNSALGHVNSTIKELRRLFLVDDLVDSLKFAVLMMYFTYVGALFNGLTLLILA 151
 2 DDQ-------KKRWK-DKVVDLLYWRDIKKTGVVFGAS 31
 32 LFLLLSLTVFSIVSVTAXIALALLSVTISFRIYKGVIQAIQKSDEGHPPRAYLESEVAIS 91
 Query Match 50.1%; Score 914; DB 1; Length 199;
Best Local Similarity 83.3%; Pred. No. 1.2e-22;
Matches 190; Conservative 3; Mismatches 5; Indels 30; Gaps
 137 Lumenal (Potential).
162 Potential.
199 Cytoplaemic (Potential).
199 Reticulon.
22466 MW; 07BESDS80059ED9C CRC64;
 Search completed: June 23, 2005, 10:55:54 Job time: 118.842 secs
 199 AA;
 DOMAIN
TRANSMEM
DOMAIN
DOMAIN
SEQUENCE
 253
 313
 FTFF
 ď
 ઠે
 셤
 ð
 a
 ઠ
```

This page Blonk (USDIO)

```
(without alignments)
882.327 Million cell updates/sec
 US-09-830-972-29-FUSED
1850
1 MEDLDQSPLVSSSDSPPRPQ......VKDAWAKIQAKIPGLKRKAE 361
 June 23, 2005, 09:47:53 ; Search time 30.5423 Seconds
 513545
GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
 Issued Patents AA:*

'cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
'cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
'cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
'cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
'cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
'cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
 Total number of hits satisfying chosen parameters:
 513545 seqs, 74649064 residues
 Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
 OM protein - protein search, using sw model
 BLOSUM62
Gapop 10.0 , Gapext 0.1
 Minimum DB seq length: 0
Maximum DB seq length: 2000000000
 Title:
Perfect score:
 Scoring table:
 Sequence:
 Searched:
 Database
 Run on:
```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

|   | Description              | Sequence 1, Appli |                    |                 |                    |                    | 9               | 7               | Sequence 8, Appli | 88                 |                    |                   | Sequence 3, Appli |                     |                    | Sequence 4601, Ap  |                     | Sequence 411, App | 1175                | 7               | Sequence 2, Appli | ď               | 4               | H               | Sequence 4, Appli | 786                 |                    | 9768.              |
|---|--------------------------|-------------------|--------------------|-----------------|--------------------|--------------------|-----------------|-----------------|-------------------|--------------------|--------------------|-------------------|-------------------|---------------------|--------------------|--------------------|---------------------|-------------------|---------------------|-----------------|-------------------|-----------------|-----------------|-----------------|-------------------|---------------------|--------------------|--------------------|
|   | ID                       | US-08-700-607-1   | US-09-949-016-9124 | US-08-700-607-5 | US-09-949-016-6998 | US-09-949-016-9180 | US-08-700-607-6 | US-08-700-607-7 | US-08-700-607-8   | US-09-949-016-8859 | US-09-949-016-7290 | US-09-149-476-563 | US-08-700-607-3   | US-09-270-767-45132 | US-09-621-976-4600 | US-09-621-976-4601 | US-09-513-999C-6304 | US-09-149-476-411 | US-09-902-540-11750 | US-09-080-897-2 | US-09-323-735-2   | US-08-899-595-3 | US-09-080-897-4 | US-08-899-595-1 | US-09-323-735-4   | US-09-513-999C-7861 | US-09-538-092-1081 | US-09-949-016-9768 |
|   | DB                       | 2                 | 4                  | ~               | 4                  | 4                  | ~               | ~               | ~                 | 4                  | 4                  | 4                 | ~                 | 4                   | 4                  | 4                  | 4                   | 4                 | 4                   | 0               | ٣                 | m               | ~               | ო               | m                 | 4                   | 4                  | 4                  |
|   | Query<br>Match Length DB | 199               | . 201              | 176             | 176                | 439                | 356             | 208             | 267               | 192                | 588                | 168               | 241               | 219                 | 75                 | 75                 | 68                  | 92                | 1027                | 1248            | 1248              | 1315            | 1255            | 1255            | 1255              | 114                 | 2090               | 2120               |
| ф | Query<br>Match           | 50.1              | 50.1               | 44.7            | 44.7               | 43.5               | 42.7            | 37.0            | 36.0              | 33.9               | 32.4               | 29.3              | 29.1              | 28.0                | 18.9               | 18.9               | 18.8                | 15.4              | 14.9                | 14.0            | 14.0              | 14.0            | 13.9            | 13.9            | 13.9              | 13.4                | 13.4               | 13.4               |
|   | Score                    | 927               | 927                | 827.7           | 827.7              | 804.9              | 789.8           | 684.2           | 999               | 627.9              | 599.1              | 541.9             | 538.3             | 518                 | 348.9              | 348.9              | 347                 | 285               | 276.2               | 259.7           | 259.7             | 258.2           | 256.5           | 256.5           | 256.5             | 248.2               | 247                | 247                |
|   | Result<br>No.            | 7                 | 8                  | m               | 4                  | S                  | 9               | 7               | œ                 | 6                  | 10                 | 11                | 12                | 13                  | 14                 | 15                 | 16                  | 17                | 18                  | 19              | 20                | 21              | 22              | 23              | 24                | 25                  | 26                 | 27                 |

| Sequence 32, Appl | Sequence 22, Appl | Sequence 2, Appli | Sequence 10562, A   | Sequence 4, Appli | Sequence 4, Appli | Sequence 4, Appli  | Sequence 4, Appli | Sequence 4, Appli | Sequence         | -                | Sequence            | -,                  | Sequence 2,     | Sequence 2, Appli | Sequence 2,      | Sequence 2, Appli | Sequence 2, Appli |
|-------------------|-------------------|-------------------|---------------------|-------------------|-------------------|--------------------|-------------------|-------------------|------------------|------------------|---------------------|---------------------|-----------------|-------------------|------------------|-------------------|-------------------|
| US-08-714-741-32  | US-08-922-635-22  | US-09-364-206-2   | US-09-949-016-10562 | US-08-459-568-4   | US-08-399-411-4   | · US-08-516-859A-4 | US-09-586-472-4   | US-09-528-706-4   | US-08-764-870-14 | US-08-980-115-14 | US-09-949-016-11382 | US-09-949-016-11383 | US-08-459-568-2 | US-08-399-411-2   | US-08-516-859A-2 | US-09-586-472-2   | US-09-528-706-2   |
| 4                 | m                 | 4                 | 4                   | 7                 | ~                 | ო                  | m                 | 4                 | ო                | ო                | 4                   | 4                   | ~               | N                 | m                | m                 | 4                 |
| 8991              | 1070              | 1504              | 990                 | 1719              | 1719              | 1719               | 1719              | 1719              | 933              | 933              | 1540                | 1540                | 1706            | 1706              | 1706             | 1706              | 1706              |
| 13.3              | 13.3              | 13.3              | 13.2                | 13.2              | 13.2              | 13.2               | 13.2              | 13.2              | 13.1             | 13.1             | 12.9                | 12.9                | 12.9            | 12.9              | 12.9             | 12.9              | 12.9              |
| 246.1             | 245.8             | 245.8             | 244.5               | 243.6             | 243.6             | 243.6              | 243.6             | 243.6             | 241.5            | 241.5            | 238.7               | 238.7               | 238.7           | 238.7             | 238.7            | 238.7             | 238.7             |
| 28                | 53                | 30                | 31                  | 32                | 33                | 34                 | 32                | 36                | 37               | 38               | 39                  | 40                  | 41              | 42                | 43               | 44                | 45                |
|                   |                   |                   |                     |                   |                   |                    |                   |                   |                  |                  |                     | •                   |                 |                   |                  |                   |                   |

## ALIGNMENTS

```
Gaps
 ö
 Query Match 50.1%; Score 927; DB 2; Length 199; Best Local Similarity 100.0%; Pred. No. 1.1e-33; Matches 188; Conservative 0; Mismatches 0; Indels
 GENERAL INFORMATION:
APPLICANT: Bandman, Olga
APPLICANT: Au-Young, Janice
APPLICANT: Goli, Surya K.
APPLICANT: Hillman, Jennifer L.
TITLE OF INVENTION: TWO NOVEL HUMAN NSP-LIKE PROTEINS
NUMBER OF SEQUENCES: 9
CORRESPONDENCES: 9
CORRESPONDENCES: Incyte Pharmaceuticals, Inc.
 3: Incyte Pharmaceuticals, Inc.
3174 Porter Drive
 COMPUTER: IBM Compatible OPERATING SYSTEM: DOS SOFTWARE: FastSEQ Version 1.5 SOURRENT APPLICATION DATA: US/08/700,607 FILING DATE: Filed Herewith ATTORNEY/AGENT INFORMATION:
; Sequence 1, Application US/08700607; Patent No. 5858708
 COUNIAL.
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
 36,749
 REFERENCE/DOCKET NUMBER: PE
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
 199 amino acids
 NAME: Billings, Lucy J
REGISTRATION NUMBER: 3
 TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS
 415-845-4166
 Consensus
 amino acid
 STREET: 31/2 ...
 linear
 IMMEDIATE SOURCE:
 STRANDEDNESS:
 MOLECULE TYPE:
 TOPOLOGY:
 STATE: C. COUNTRY:
 LIBRARY:
 CLONE: C
US-08-700-607-1
 LENGTH:
```

174 VVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQAI 233

ઠે

ö

ò d

```
-STVPAPSPLSAAAVSP 130
 70 ÓSPVAMETASTGVAGVSSAMDHTFSTTSKDGEGSCYTSLISDICYPPQEDSTYFTGILQK 129
 130 ENGHVTISESPEELGTPGPSLPDVPGIESRGLFSSDSGIEMTPAESTEVNKILADPLDQM 189
 250 IKDHLLEESTFAPYIDDLSEEQRRAPQITTPVKITLTEIEPSVETTTQEKTPEKQDICLK 309
 310 PSPDTVPTVTVSEPEDDSPGSITPPSSGTEPSAAESQGKGSISEDELITAIKEAKGLSYE 369
 370 TAENPRPVGQLADRPEVKARSGPPTIP---SPLDHEASSAESGDSEIELVSEDPMAAEDA 426
 427 LPSGYVSFGHVGGPP----PSPASPSIQYSILREEREAELDSELIIESCDASSASEESPK 482
 131 SKLPEDD-----EPPARPPPPPASVSPQAEPVWTPPAP-APAAPP-----STSVVDLL
 --VLERKPAAGLS--
 Gaps
 Indels 383;
 483 REQDSPPMKPSALDAIREETGVRAEERAPSRRGLAEPGSFLDYPSTEPQPGP
 Length 776;
 22 ---AFKYQFVREPEDEEEEEEEEEDEDEDLE-----
 ; Score 827.7; DB 2;
; Pred. No. 3.6e-28;
55; Mismatches 89;
 79 ----MDFGNDFVPPAPRGPLPAAPPV-----
 ------PTAPAAGAPL-
 CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc. STREET: 3174 Porter Drive CITY: Palo Alto
 COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/700,607
FILING DATE: Filed Herewith
ATTORNEY/AGENT INFORMATION:
 PF-0114 US
 10 ----VSSSDSPPR---PQP----
 NAME: Billings, Lucy J. REGISTRATION NUMBER: 36,749
 REFERENCE/DOCKET NUMBER: PF
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
 44.78;
27.18;
 COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
 776 amino acids
 104 RQ---PSWDPSPVS---
 Best Local Similarity 27.1
Matches 196; Conservative
 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS
 TOPOLOGY: linear MOLECULE TYPE: peptide IMMEDIATE SOURCE:
 65 ----AAPV----
 LIBRARY: GenBank
CLONE: 307307
 amino acid
 u.s.
 OSPL---
 STRANDEDNESS:
 94304
 S
 CITY: Pa
STATE: C
COUNTRY:
 US-08-700-607-5
 LENGTH:
 9
 Query Match
 21
 54
 ਨੋ
 ద
 ò
 g
 ò
 요
 à
 셤
 ŏ
 셤
 à
 a
 ò
 셤
 ઠે
 셤
 ò
 | SENERAL INFORMATION:
| APPLICANT: VENTER, J. Craig et al. |
| APPLICANT: VENTER, J. Craig et al. |
| APPLICANT: VENTER, J. Craig et al. |
| TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
| TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
| FILE REPERENCE: CLOO1307 |
| CURRENT APPLICATION NUMBER: US/09/949, 016 |
| PRIOR APPLICATION NUMBER: 60/241, 755 |
| PRIOR FILING DATE: 2000-10-20 |
| PRIOR FILING DATE: 2000-10-03 |
| PRIOR FILING DATE: 2000-10-03 |
| PRIOR FILING DATE: 2000-09-08 |
| NUMBER OF SEQ ID NOS: 207012 |
| SEGPIN APPLICATION NUMBER: 60/231, 498 |
| NUMBER OF SEQ ID NOS: 207012 |
| SEGPIN APPLICATION NUMBER: 100/2016 |
| SEG ID NO 9124 |
| LENGTH: 201
 ö
 174 VVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQAI 233
 134 MWVFTYVGALFNGLTLILIALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAKI 193
 234 QKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDSLKFAVL 293
 72 QKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDSLKFAVL 131
 294 MWVFTYVGALFNGLTLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAKI 353
 132 MWVFTYVGALFNGLTLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAXI 191
 234 QKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDSLKFAVL 293
 74 QKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDSLKFAVL 133
 294 MWVFTYVGALFNGLTLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAKI 353
 73
 71
12 VVDLYWRDIKKTGVVFGASLFLLLSLIVFSIVSVTAYIALALLSVTISFRIYKGVIQAI
 14 VVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQAI
 Gaps
 ;
0
 Length 201;
 Indels
 APPLICANT: Bandman, Olga
APPLICANT: Au-Young, Janice
APPLICANT: Goli, Surya K.
APPLICANT: Hillman, Jennifer L.
TITLE OF INVENTION: TWO NOVEL HUMAN NSP-LIKE PROTEINS
NUMBER OF SEQUENCES: 9
 50.1%; Score 927; DB 4; L
100.0%; Pred. No. 1.1e-33;
ive 0; Mismatches 0;
 Sequence 9124, Application US/09949016
Patent No. 6812339
 Sequence 5, Application US/08700607
Patent No. 5858708
GENERAL INFORMATION:
 Query Match
Best Local Similarity 100.(
Matches 188; Conservative
 PGLKRKAE 199
 PGLKRKAE 361
 PGLKRKAE 361
 PGLKRKAE 201
 TYPE: PRT ORGANISM: Human
 US-09-949-016-9124
 US-09-949-016-9124
 US-08-700-607-5
 354
 354
 g
 ઠે
 셤
 ò
 d
 유
 ð
 움
 ò
 g
```

ਨੇ

ò

17;

| Db 427 LPSGYVSPGHVGGPPPSPASPSIQYSILREBREAELDSELIIESCDASSASEESPK 482  Qy 104 RQPSWDPSPVS                                                                                                                                                                                                                                                 | Qy       299 YVGALFNGLTLLILALISLESVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAKI PGLKR 358         Db       714 YVGALFNGLTLLLMAVVSMFTLPVVYVKHQAQIDQYLGLVRTHINAVVAKIQAKI PGAKR 773         Qy       359 KAE 361         Db       774 HAE 776    RESULT 5 | 949-016-9180 ence 9180, Application US/099490 nt NO. 681233 RAL INFORMATION: LICANT: VENTER, J. Craig et al. LICONI: VENTER, J. Craig et al. LE OF INVENTION: POLYMORPHISMS ILE OF INVENTION: WITH HUMAN DIS E REFERENCE: CL001307 ERNT APPLICATION NUMBER: 60/241, 75 OR APPLICATION NUMBER: 60/241, 75 OR RELING DATE: 2000-10-20 OR PILING DATE: 2000-10-03 OR FILING DATE: 2000-10-03 | FRLOK PELLICALION NUMBER: 60/231,498                                                                                                                                       | Query Match         43.5%;         Score 804.9;         DB 4;         Length 439;           Best Local Similarity         40.9%;         Pred. No. 1.2e-27;         Adches 111;         Caps 111;           Matches 177;         Conservative         48;         Mismatches 97;         Indels 111;         Caps 11;           Qy         4 LDQSPLVSSDSPRRQPAFKYQFVRPEBEBEBEBEBEBEBEBEBEBEBELEUERKPAAGL 63         1 | 0.00   0.00   0.00   0.00   0.00   0.00   0.00   0.00   0.00   0.00   0.00   0.00   0.00   0.00   0.00   0.00   0.00   0.00   0.00   0.00   0.00   0.00   0.00   0.00   0.00   0.00   0.00   0.00   0.00   0.00   0.00   0.00   0.00   0.00   0.00   0.00   0.00   0.00   0.00   0.00   0.00   0.00   0.00   0.00   0.00   0.00   0.00   0.00   0.00   0.00   0.00   0.00   0.00   0.00   0.00   0.00   0.00   0.00   0.00   0.00   0.00   0.00   0.00   0.00   0.00   0.00   0.00   0.00   0.00   0.00   0.00   0.00   0.00   0.00   0.00   0.00   0.00   0.00   0.00   0.00   0.00   0.00   0.00   0.00   0.00   0.00   0.00   0.00   0.00   0.00   0.00   0.00   0.00   0.00   0.00   0.00   0.00   0.00   0.00   0.00   0.00   0.00   0.00   0.00   0.00   0.00   0.00   0.00   0.00   0.00   0.00   0.00   0.00   0.00   0.00   0.00   0.00   0.00   0.00   0.00   0.00   0.00   0.00   0.00   0.00   0.00   0.00   0.00   0.00   0.00   0.00   0.00   0.00   0.00   0.00   0.00   0.00   0.00   0.00   0.00   0.00   0.00   0.00   0.00   0.00   0.00   0.00   0.00   0.00   0.00   0.00   0.00   0.00   0.00   0.00   0.00   0.00   0.00   0.00   0.00   0.00   0.00   0.00   0.00   0.00   0.00   0.00   0.00   0.00   0.00   0.00   0.00   0.00   0.00   0.00   0.00   0.00   0.00   0.00   0.00   0.00   0.00   0.00   0.00   0.00   0.00   0.00   0.00   0.00   0.00   0.00   0.00   0.00   0.00   0.00   0.00   0.00   0.00   0.00   0.00   0.00   0.00   0.00   0.00   0.00   0.00   0.00   0.00   0.00   0.00   0.00   0.00   0.00   0.00   0.00   0.00   0.00   0.00   0.00   0.00   0.00   0.00   0.00   0.00   0.00   0.00   0.00   0.00   0.00   0.00   0.00   0.00   0.00   0.00   0.00   0.00   0.00   0.00   0.00   0.00   0.00   0.00   0.00   0.00   0.00   0.00   0.00   0.00   0.00   0.00   0.00   0.00   0.00   0.00   0.00   0.00   0.00   0.00   0.00   0.00   0.00   0.00   0.00   0.00   0.00   0.00   0.00   0.00   0.00   0.00   0.00   0.00   0.00   0.00   0.00   0.00   0.00   0.00   0.00   0.00   0.00   0.00   0.00   0.00   0.00   0.00   0.00   0.00   0.00   0.00   0.00   0.00 |
|-----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|---------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|-------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|----------------------------------------------------------------------------------------------------------------------------------------------------------------------------|-----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|---------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| Qy         179 YWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAXIALALLSVTISFRIYKGVIQALQKSDE         238           Db         594 YWRDIKCTGIVFGSFLLLLFRELTQFSVVSVVAXIALAALSATISFRIYKSVLQAVQKTDE         653           Qy         239 GHPFRAYLESELVQKYSNSALGHVNCTIKELRRLFLVDDLVDSLKFAVLMMVFT         298           I  :   :  :  :  :  : : : : : : : : : : | 13 x Pc                                                                                                                                                                                                                                     | ; CURRENT FILING DATE: 2000-04-14 ; PRIOR APPLICATION NUMBER: 60/241,755 ; PRIOR PILING DATE: 2000-10-20 ; PRIOR PILING DATE: 2000-110-03 ; PRIOR PILING DATE: 2000-09-08 ; PRIOR FILING DATE: 2000-09-08 ; PRIOR FILING DATE: 2000-09-08 ; NUMBER OF SEQ ID NOS: 207012 ; SOFTWARE: FastSEQ for Windows Version 4.0 ; SEQ ID NO 6998 ; TYPE: PRT ; ORGANISM: Human US-09-949-016-6998    | Query Match  44.7%; Score 827.7; DB 4; Length 776;  Best Local Similarity 27.1%; Pred. No. 3.6e-28;  Matches 196; Conservative 55; Mismatches 89; Indels 383; Gaps  6 QSPL | 10VSSSDSPRPQP                                                                                                                                                                                                                                                                                                                                                                                                         | 1   250 IXDHLLEESTFAPYIDDLSEEQRRAPQITTPVKITLTEIEPSVETTTQEKTPEKQDICLK 309   1   250 IXDHLLEESTFAPYIDDLSEEQRRAPQITTPVKITLTEIEPSVETTTQEKTPEKQDICLK 309   254                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 |

```
200 VVSVVAYLALAALSATISFRIYKSVLQAVQKTDEGHPFKAYLELEITLSQEQIQKYTDCL 259
 260 QFYVNSTLKELRLFLVQDLVDSLKFAVLMMLLTYVGALFNGLTLLLMAVVSMFTLPVVY 319
 104 RQPS----WDPS---PVSSTVPAPSPLSAAAVSPSKLPEDD-----EPPARPPPPASV 151
 89 RAPSRRGLAEPGSFLDYPSTEPQPGP-----ELPPGDGALEPETPMLPRKPEEDSS 139
 28
 152 SPQAEPVWTPPAP-APAAPP----STSVVDLLYWRDIKKTGVVFGASLFLLLSLTVFS
 265 LGHVNCTIKELRRIFLVDDLVDSLKRAVLMWVFTYVGALFNGLTLLILALISLFSVPVIY
 152 SPQAEPVWTPPAPPAPPAPPSTSVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAY
 Length 208;
 Indels
 GENERAL INFORMATION:

APPLICANT: Bandman, Olga
APPLICANT: Au-Young, Janice
APPLICANT: Goli, Surya K.
APPLICANT: Hillman, Jennifer L.
TITLE OF INVENTION: TWO NOVEL HUMAN NSP-LIKE PROTEINS
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
 320 VKHQAQIDQYLGLVRTHINAVVAKIQAKIPGAKRHAE 356
 325 ERHQAQIDHYLGLANKNVKDAMAKIQAKIPGLKRKAE 361
 Query Match 37.0%; Score 684.2; DB 2; Best Local Similarity 62.4%; Pred. No. 6.7e-23; Matches 131; Conservative 35; Mismatches 36;
 E: Incyte Pharmaceuticals, Inc.
3174 Porter Drive
 SOFTWARE: FastSEQ Version 1.5
CUBRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/700,607
FILING DATE: Filed Herewith
ATTORNEY AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36.74°
TEFFENCE/DOCKFT.
 Sequence 7, Application US/08700607
Patent No. 5858708
 TELECOMMUNICATION INFORMATION
 E: Diskette
IBM Compatible
 LENGTH: 208 amino acids
TYPE: amino acid
STRANDEDNESS: single
 TELEPHONE: 415-855-0555
 ZIP: 94304
COMPUTER REALABLE FORM:
MEDIUM TYPE: Dieber
 TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO:
 SEQUENCE CHARACTERISTICS LENGTH: 208 amino acid
 linear
 Palo Alto
 IMMEDIATE SOURCE:
 307311
 TOPOLOGY: 11
MOLECULE TYPE:
 LIBRARY:
 US-08-700-607-7
 STREET:
 셤
 ò
 В
 ò
 요
 ઠ
 ò
 셤
 8
 a
 10;
247 INKQKAIDLLYWRDIKQTGIVFGSFLLLLFSLTQFSVVSVVAYLALAALSATISFRIYKS 306
 KFAVLMWVFTYVGALFNGLTLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAK 348
 229 VIQAIQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDSL 288
 16 PPRP-QPAFKYQFVREPEDEE-------EEEEEEEEEDEDEDLEELEVLERK 58
 ----SPPMKPSALDAIREETGVRAEE 88
 Indels 112;
 Length 356;
 GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT:
AP
 59 PAAGLSAAPVPTAPAAGAPLMDFGNDFVPPAPRGPLPAAPPVAP---
 21 PPSPASPSIOYSILREEREAELDSELIIESCDASSASEESPKREOD
 DB 2;
 Score 789.8; DB 2
Pred. No. 3.9e-27;
 42; Mismatches
 COMPUTER READBALE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEO Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/700,607
FILING DATE: Filed Herewith
ATTORNEY/AGENT INFORMATION:
NAMME: Billings, Lucy J:
REGISTRATION NUMBER: 36,749
 REFERENCE/DOCKET NUMBER: PF-0114 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
 42.7%;
 LENGTH: 356 amino acida
TYPE: amino acid
STRANDEDNESS: single
 427 İQAKİPGAKRHAE 439
 349 IQAKIPGLKRKAE 361
 Query Match
Best Local Similarity 42.69
Matches 169; Conservative
 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
 TOPOLOGY: linear
MOLECULE TYPE: peptide
IMMEDIATE SOURCE:
 MEDIALI
LIBRARY: Genbur
 u.s.
 COUNTRY: U
ZIP: 94304
 02-08-700-607-6
 0S-08-700-607-6
 289
 g
 셤
 ò
 à
 ò
 셤
 g
 ò
```

g ઠે 요 ò a

```
Sequence 7290, Application US/09949016

Patent No. 6812339
GENERAL INPORMATION:
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CLOO1307
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/231,768
PRIOR PILING DATE: 2000-10-20
PRIOR PLING DATE: 2000-10-03
PRIOR PILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-09-08
NUMBER: 6 6 7237,768
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-10-03
SPRIOR FILING DATE: 2000-10-03
SPRIOR FILING DATE: 2000-09-08
NUMBER: FAST DE CONTOLO NOW WERE
SEQ ID NOS: 207012
SOFTWARE: FAST SEQ FOR WINDOWS VERSION 4.0
 APPLICANT: VENTER, J. Craig et al.

APPLICANT: VENTER, J. Craig et al.

IIILE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

IIILE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

FILE REFERENCE: CLOO1307

CURRENT APPLICATION: NUMBER: US/09/949,016

CURRENT APPLICATION NUMBER: US/09/949,016

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR FILING DATE: 2000-10-20

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-01-08

SRIOR APPLICATION NUMBER: 60/231,498

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOFTWARRE: FastSEQ for Windows Version 4.0

SEQ ID NO 8859
 173 SVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQA 232
 123 FWHLMTYVGAVFNGITLLILAELLIFSVPIVYEKYKTQIDHYVGIARDQTKSIVEKIQAK 182
130 VLMWLLTYVGALFNGLTLLLMAVVSMFTLPVVYVKHQAQVDQYLGLVRTHINTVVAKIQA 189
 233 IQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDSLKFAV 292
 293 LMWVFTYVGALFNGLTLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAK 352
 3 SVHDLIFWRDVKKTGFVFGTTLIMLLSLAAFSVISVVSYLILALLSVTISFRIYKSVIQA 62
 Length 192;
 Indels
 33.9%; Score 627.9; DB 4;
61.1%; Pred. No. 1.8e-20;
tive 38; Mismatches 35;
 ; Sequence 8859, Application US/09949016; Patent No. 6812339; GENERAL INFORMATION:
 Query Match
Best Local Similarity 61.11
Matches 116; Conservative
 :||: |:|||
183 LPGIAKKKAE 192
 353 IPGL-KRKAE 361
 352 KIPGLK 357
 190 KIPGAR 195
 Human
 JS-09-949-016-8859
 US-09-949-016-8859
 US-09-949-016-7290
 TYPE: PRT
 용
셤
 ò
 셤
 셤
 ઠે
 ద
 ð
 ઠ
 331
 172 TSVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQ 231
 232 AIQKSDEGHPFRAYLESEVAISEELVQXYSNSALGHVNCTIKELRRLFLVDDLVDSLKFA 291
 292 VLMWVFTYVGALFNGLTLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQA 351
 10 SQAIDLLYWRDIKQTGIVFGSFLLLLFSLTQFSVVSVVAYLALAALSATISFRIYKSVLQ 69
 212 IALALLSVTISFRIYKGVIQAIQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNCT
 0; Gaps
 GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: Bandman, Olga

APPLICANT: Bandman, Olga

APPLICANT: Hillman, Jannice

APPLICANT: Hillman, Jennifer L.

TITLE OF INVENTION:

NUMBER OF SEQUENCE: 9

CORRESPONDENCE ADDRESS:

ADDRESSEE: Incyte Pharmaccuticals, Inc.

STREET: 3174 Porter Drive

CITY: Palo Alto
 Length 267;
 29; Indels
 Query Match 36.0%; Score 666; DB 2; Best Local Similarity 66.1%; Pred. No. 6.8e-22; Matches 123; Conservative 34; Mismatches 29
 | |||| :: :|||||||| || ||| DQYLGLVRTHINAVVAKIQAKIPGAKRHAE 208
 DHYLGLANKNVKDAMAKIQAKIPGLKRKAE 361
 COMPUTER TYPE: Diskette
COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
SOFTWARE: FastSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/700,607
FILING DATE: Filed Herewith
ATTORNEY/AGENT INFORMATION:
NAMME: Billings, Lucy J.
REGISTRATION NUMBER: PF-0114 US
TELEPHONE: 415-85-055
TELEPHONE: 415-85-055
TELEPHONE: 415-85-055
TELEPHONE: 415-85-055
TELEPHONE: AIS-85-055
STELEPHONE: AIS-85-055
TELEPHONE: AIS-85-055
STELEPHONE: AIS-85-055
TELEPHONE: AIS-85-055
STELEPHONE: AIS-85-055
TELEPHONE: AIS-85-055
TELEPHONE: AIS-85-055
TELEPHONE: AIS-85-055
 LENGTH: 267 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
 ZIP: 94304
COMPUTER READABLE FORM:
 LIBRARY: General Control Contr
 u.s.
 COUNTRY:
 US-08-700-607-8
 332
```

셤

셤 ò

```
EARLIER I
EARLIER I
 ||:||| :|
76 DFRELHTAREFSEEDBEETTSQDWGTPRELTFSYIAFDGVVGSGGRRDSTARRPRPQGRS 135
 +48S AATQLRHFFLVEDLVDSLKLALLFYILFFVGAIFNGLTLLILGVIGLFTIPLLYRQHQAQ 544
 RG------QPSWDP----SPV 113
 195 RĠTGSGEDSSTSSSTPLEDEEPQEPNRLETGEAGEELDLRLRLAQPS-SPEVLTPQLSPG 253
 308 TVEPRLLGTAMEWLKTSLLLAVYKTVPILELSP---PLWTAIGWVORGPTPVTRVLL 364
 211 YIALALLSVTISFRIYKGVIQAIQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNC 270
 271 TIKELRRLFLVDDLVDSLKFAVLMWVFTYVGALFNGLTLLILALISLFSVPVIYERHQAQ 330
 --PAFKYQFVRE-----35
 18 DERPRPRAGGGTAGVGGGPDAGPRGAMGQVLPVFAH--CKEAPSTASSTPDSTEGGNDDS 75
 47 ------BDLEELEVLERKPAAGLSAAPVPTAPAAGAPLMD--FGNDFVPPAP 90
 163 ----APAPAAPPSTS-----VVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTA
 Gaps
 ; Score 599.1; DB 4; Length 588;
; Pred. No. 2.8e-18;
56; Mismatches 122; Indels 249;
 545 IDQYVGLVTNQLSHIKAKIRAKIPGTGALASAAAAVSGSKAKAE 588
 331 IDHYLGLANKNVKDAMAKIQAKIPGL-------KRKAE 361
 Sequence 563, Application US/09149476
Patent No. 6420526
GENERAL INFORMATION:
APPLICANT: ROSEN et al.
TITLE OF INVENTION: 186 Human Secreted proteins
FILE REFERENCE: PZ002P1
CURRENT FILING DATE: 1998-09-08
EARLIER APPLICATION NUMBER: PCT/US98/04493
EARLIER APPLICATION NUMBER: 60/040,162
EARLIER APPLICATION NUMBER: 60/040,162
EARLIER APPLICATION NUMBER: 60/040,162
EARLIER APPLICATION NUMBER: 60/040,162
EARLIER FILING DATE: 1997-03-07
EARLIER FILING DATE: 1997-03-07
EARLIER FILING DATE: 1997-03-07
 114 SSTVPAPSPLSAAAVSPSKLPEDDEPPARP------
 36 -----36 EEEEEEEDED------
 R APPLICATION NUMBER: 60/038,621
R FILING DATE: 1997-03-07
R APPLICATION NUMBER: 60/040,626
R FILING DATE: 1997-03-07
R FILING DATE: 1997-03-07
R FILING DATE: 1997-03-07
R APPLICATION NUMBER: 60/040,336
 32.4%;
26.9%;
 Query Match
Best Local Similarity 26.9
Matches 157; Conservative
 14 DSPPRPQ-----
; LENGTH: 588
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-7290
 RESULT 11
US-09-149-476-563
 91
 EARLIER I
EARLIER I
 EARLIER
EARLIER
EARLIER
EARLIER
EARLIER
 셤
 g
 요
 ò
 음
 ઠે
 g
 ò
 ద
 셤
 à
 ద
 g
 ò
 8
 ઠ
```

à

ઠે

APLIING DATE: 1997-05-23
APPLICATION NUMBER: 60/047,581 APPLICATION DATE: 1997-05-23
APPLICATION NUMBER: 60/047,582
APPLICATION NUMBER: 69/047,582 APPLICATION NUMBER: 60/047,596 FILING DATE: 1997-05-23 APPLICATION NUMBER: 60/047,612 FILING DATE: 1997-05-23 APPLICATION NUMBER: 60/047,615 FILING DATE: 1997-05-23 APPLICATION NUMBER: 60/043,313 FILING DATE: 1997-04-11 APPLICATION NUMBER: 60/048,974 FILING DATE: 1997-06-06 APPLICATION NUMBER: 60/047,600 FILING DATE: 1997-05-23 APPLICATION NUMBER: 60/047,633 FILING DATE: 1997-05-23 FILING DATE: 1997-05-23 APPLICATION NUMBER: 60/047,583 APPLICATION NUMBER: 60/047,617 FILING DATE: 1997-05-23 APPLICATION NUMBER: 60/047,592 APPLICATION NUMBER: 60/047,584 FILING DATE: 1997-05-23 APPLICATION NUMBER: 60/047,587 FILING DATE: 1997-05-23 APPLICATION NUMBER: 60/047,613 APPLICATION NUMBER: 60/043,568 FILING DATE: 1997-04-11 APPLICATION NUMBER: 60/043,314 :CATION NUMBER: 60/043,569 APPLICATION NUMBER: 60/043,669 APPLICATION NUMBER: 60/043,312 APPLICATION NUMBER: 60/047,597 APPLICATION NUMBER: 60/047,502 APPLICATION NUMBER: 60/047,618 APPLICATION NUMBER: 60/047,503 APPLICATION NUMBER: 60/047,500 APPLICATION NUMBER: 60/047,492 APPLICATION NUMBER: 60/047,598 APPLICATION NUMBER: 60/047,632 APPLICATION NUMBER: 60/047,601 APPLICATION NUMBER: 60/043,580 APPLICATION NUMBER: 60/043,311 APPLICATION NUMBER: 60/043,671 APPLICATION NUMBER: 60/043,674 1997-05-23 1997-05-23 1997-05-23 1997-05-23 1997-05-23 1997-05-23 1997-05-23 1997-05-23 1997-05-23 1997-05-23 1997-04-11 1997-04-11 1997-05-2 1997-04-1 1997-04-1 1997-04-1 1997-04-1 1997-04-1 1997-03-0 1997-04-1 1997-04-1 LING DATE: LING DATE: LING DATE: LING DATE: LING DATE: FILING DATE: LING DATE:

```
R APPLICATION NUMBER: 60/056, 880
R FILING DATE: 1997-08-22
R APPLICATION NUMBER: 60/056, 894
R PILING DATE: 1997-08-22
R APPLICATION NUMBER: 60/056, 911
R PILING DATE: 1997-08-22
R APPLICATION NUMBER: 60/056, 636
R PILING DATE: 1997-08-22
R PELING DATE: 1997-08-22
R PILING DATE: 1997-08-22
 REFLING DATE: 1997-08-22

REPLING DATE: 1997-08-23

REPLING DATE: 1997-05-23

 FILING DATE: 1997-08-22
APPLICATION NUMBER: 60/056,893
FILING DATE: 1997-08-22
APPLICATION NUMBER: 60/056,630
FILING DATE: 1997-08-22
 FILING DATE: 1997-08-22
APPLICATION NUMBER: 60/056,889
 APPLICATION NUMBER: 60/056,878
 FILING DATE: 1997-08-22
APPLICATION NUMBER: 60/056,662
FILING DATE: 1997-08-22
 APPLICATION NUMBER: 60/056,872
FILING DATE: 1997-08-22
APPLICATION NUMBER: 60/056,882
 APPLICATION NUMBER: 60/056,903
FILING DATE: 1997-08-22
APPLICATION NUMBER: 60/056,888
FILING DATE: 1997-08-22
 FILING DATE: 1997-05-23
APPLICATION NUMBER: 60/047,589
FILING DATE: 1997-05-23
APPLICATION NUMBER: 60/047,593
APPLICATION NUMBER: 60/056,886
 APPLICATION NUMBER: 60/056,637
FILING DATE: 1997-08-22
 APPLICATION NUMBER: 60/056,879
FILING DATE: 1997-08-22
 FILING DATE: 1997-05-23
APPLICATION NUMBER: 60/047,614
 APPLICATION NUMBER: 60/043,578
 FILING DATE: 1997-04-11
APPLICATION NUMBER: 60/043,576
 APPLICATION NUMBER: 60/047,501
 FILING DATE: 1997-08-22
 FILING DATE: 1997-05-23
 1997-08-2
 EARLIER
EARLIER
EARLIER
EARLIER
EARLIER
EARLIER
EARLIER
EARLIER
EARLIER
EARLIER
EARLIER
EARLIER
EARLIER
EARLIER
EARLIER
EARLIER
EARLIER
EARLIER
EARLIER
EARLIER
EARLIER
EARLIER
EARLIER
EARLIER
EARLIER
EARLIER
EARLIER
EARLIER
EARLIER
EARLIER
EARLIER
EARLIER
EARLIER
EARLIER
 EARLIER I
 EARLIER
EARLIER
EARLIER
EARLIER
EARLIER
EARLIER
EARLIER
 EARLIER
EARLIER
EARLIER
EARLIER
EARLIER
EARLIER
EARLIER
EARLIER
EARLIER
EARLIER
EARLIER
EARLIER
EARLIER
EARLIER
EARLIER
EARLIER
EARLIER
EARLIER
EARLIER
EARLIER
EARLIER
EARLIER
EARLIER
EARLIER
EARLIER
EARLIER
EARLIER
EARLIER
EARLIER
EARLIER
```

61 APHNYMDAAWVHINRALKLIIRLFLVEDLVDSLKLAVFWHLMTYVGAVFNGITLLILAEL 120 256 LVQKYSNSALGHVNCTIKELRRLFLVDDLVDSLKFAVLMMVFTYVGALFNGLTLLILALI 315 196 LILSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQAIQKSDEGHPFRAYLESEVAISEE Gaps 1; DB 4; Length 168; 316 SLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAKIPGL-KRKAE 361 29.3%; Score 541.9; DB 4; Length 60.5%; Pred. No. 8.9e-17; tive 34; Mismatches 31; Indels EARLIER FILING DATE: 1997-04-11

EARLIER FILING DATE: 1997-04-11

EARLIER FILING DATE: 1997-04-11

EARLIER APPLICATION NUMBER: 60/056,664

EARLIER APPLICATION NUMBER: 60/056,664

EARLIER FILING DATE: 1997-08-22

EARLIER FILING DATE: 1997-08-22

EARLIER FILING DATE: 1997-08-22

EARLIER FILING DATE: 1997-08-22

EARLIER PELING DATE: 1997-08-22

EARLIER APPLICATION NUMBER: 60/056,909

EARLIER FILING DATE: 1997-08-22

EARLIER FILING DATE: 1997-08-22

EARLIER FILING DATE: 1997-08-22

EARLIER FILING DATE: 1997-08-22

EARLIER APPLICATION NUMBER: 60/056,807

EARLIER APPLICATION NUMBER: 60/056,807

EARLIER PELING DATE: 1997-08-22

EARLIER PELING DATE: 1997-08-22

EARLIER PELING DATE: 1997-08-22

EARLIER FILING DATE: 1997-08-22

EARLIER PILING DATE: 1997-06-05

EARLIER PILING DATE: 1997-06-05

EARLIER APPLICATION NUMBER: 60/056,804

EARLIER PILING DATE: 1997-09-05

EARLIER APPLICATION NUMBER: 60/056,804

EARLIER PILING DATE: 1997-09-05

EARLIER APPLICATION NUMBER: 60/057,669

EARLIER APPLICATION NUMBER: 60/057,669

EARLIER APPLICATION NUMBER: 60/057,669

EARLIER APPLICATION NUMBER: 60/057,669

EARLIER APPLICATION NUMBER: 60/057,669

EARLIER APPLICATION NUMBER: 60/057,669

EARLIER APPLICATION NUMBER: 60/057,669

EARLIER APPLICATION NUMBER: 60/057,669

EARLIER APPLICATION NUMBER: 60/057,669

EARLIER APPLICATION NUMBER: 60/057,669

EARLIER APPLICATION NUMBER: 60/057,669

EARLIER APPLICATION NUMBER: 60/057,669 EARLIER APPLICATION NUMBER: 60/049,610 EARLIER FILING DATE: 1997-06-13 EARLIER APPLICATION NUMBER: 60/061,060 EARLIER FILING DATE: 1997-06-13 EARLIER APPLICATION NUMBER: 60/061,060 EARLIER FILING DATE: 1997-10-02 Query Match Best Local Similarity 60.5\* Matches 101; Conservative US-08-700-607-3 ò ઠે g ઠે ద

Sequence 3, Application US/08700607
Patent No. 5858708
GENERAL INFORMATION
ADPLICANT: Bandman, Olga
APPLICANT: All-Young, Janice
APPLICANT: Goli, Surya K.
APPLICANT: Hillman, Jennifer L.
TITLE OF INVENTION: TWO NOVEL HUMAN NSP-LIKE PROTEINS
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc. STREET: 3174 Porter Drive CITY: Palo Alto STATE: CA COUNTRY: U.S.

COMPUTER: IBM Compatible OPERATING SYSTEM: DOS

COMPUTER READABLE FORM: MEDIUM TYPE: Diskett ZIP: 94304

```
TYPE: PRT
ORGANISM: Homo sapiens
 206 NKKPE 210
 357 KRKAE 361
 NAME/KEY: UNSURE
LOCATION: 53
 NAME/KEY: UNSURE
 NAME/KEY: UNSURE
 LOCATION: 19
 297
 FEATURE:
 Š
 g
 ò
 g
 δ
 В
 ઠે
 엄
 à
 g
 ò
 g
 4,
 66 APVPTAPAAGAPLMDFGNDFVPPAPRGPLPAAPPVAPERQPSWDPSPVSSTVPAPSPLSA 125
 126 AAVSPSKLPEDDEPPARPPPPASVSPQAEPVWTPPAPAPAPAPP-----STSVVD 176
 177 LLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQAIQKS 236
 DEGHPFRAYLESEVAISEELVQKYSNSALGHVNCTIKELRRIFLVDDLVDSLKFAVLMWV 296
 297 FTYVGALFNGLTLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAKIPGL 356
 9 QSHSISSS-----SF 18
 30 ----SPGACPALGTKSCSSSCAVHD 50
 6 OSPLVSSSDSPPRPQPAFKYQFVREPEDEEEEEEEEEEDEDBDLEELEVLERKPAAGLSA 65
 RESULT 13
US-09-270-767-45132
Sequence 45132, Application US/09270767
Fatent No. 6703491
GENERAL INFORMATION:
TITLE OF INVENTION: APPLICANT: Homburs et al.
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
FILE REFERENCE: File Reference: 7326-094
CURRENT APPLICATION NUMBER: US/09/270,767
NUMBER OF SEQ ID NOS: 62517
SOFURARE: PatentIn Ver. 2.0
SSEQ ID NO 45132
LENGTH: 219
 Indels 167; Gaps
 29.1%; Score 538.3; DB 2; Length 241; 30.9%; Pred. No. 2.6e-16;
 38; Mismatches
SOFTWARE: FASESEQ Version 1.5
CURRENT PAPLICATION DATA:
APPLICATION NUMBER: US/08/700,607
FILING DATE: Filed Herewith
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy,
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: 9F-0114 US
TELECOMMUICATION INFORMATION:
TELECHONE: 415-855-0555
 ; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-09-270-767-45132
 Query Match
Best Local Similarity 30.99
Matches 112; Conservative
 19 GAEPSAPGGGG-----
 357 KRK 359
 211 ROK 213
 ò
 g
 ò
 ď
 ò
 g
 8
 g
 ઠ
 qq
 ò
 뭐
 ઠે
 g
```

```
FTYVGALFNGLTLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAKIPGL 356
 ----EDLEELEVLERKPA 49
 26 LIYWRDVKKSGIVFGAGLITLAAISSFSVISVPAYLSLLTLFGTVAFRIYKSVTQAVQKT
 237 DEGHPPRAYLESEVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDSLKFAVLMWV
 1 MEDLDQSPLVSSSDSPPRPQPAFKYQFVREPEDEBEBEBEBEBEBDEDLBELEVLERKPA
 177 LLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQAIQKS
 Gaps
 Gaps
 11;
 ;
0
 DB 4; Length 75;
Query Match 28.0%; Score 518; DB 4; Length 219; Best Local Similarity 51.4%; Pred. No. 1.7e-15; Matches 95; Conservative 42; Mismatches 48; Indels
 Indels
 APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: JODGET, S.
TITLE OF INVENTION: ESTS and Encoded Human Proteins.
TITLE OF INVENTION: ESTS and Encoded Human Proteins.
CURRENT FILIGATION NUMBER: US/09/621,976
CURRENT PILIGATION NUMBER: 2000-07-21
NUMBER OF SEQ ID NOS: 19335
SOFTMARE: Patent.pm
LENGTH: 75
 Query Match
18.9%; Score 348.9; DB 4.
Best Local Similarity 82.6%; Pred. No. 6.8e-09;
Matches 71; Conservative 0; Mismatches 4.
 1 MEDLDQSPLVSSSDSPPRXQPAFKYQFXREPEDEE
 61 AGLSAAPVPTAPAAGAPLMDFGNDFV 86
 50 AGLXAAPVXTAPAAGAPLMDFGNDFV 75
 RESULT 15
US-09-621-976-4601
Sequence 4601, Application US/09621976
Perent No. 6639063
GENERAL INFORMATION:
 LOCATION: 58
OTHER INFORMATION: Xaa = His, Pro
NAME/KEY: UNSURE
LOCATION: 28
OTHER INFORMATION: Xaa = Met, Val
 OTHER INFORMATION: Xaa = Pro, Gln
 ; OTHER INFORMATION: Xaa = Ser, Tyr
US-09-621-976-4600
```

Search completed: June 23, 2005, 10:17:49 Job time: 32.5423 secs

This Page Blank (Uspto)

protein

ĕ

Run on:

Sequence:

Searched:

Database

```
61 AGLSAAPVPTAPAAGAPLMDFGNDFVPPAPRGPLPAAPPVAPERQPSWDPSPVSSTVPAP 120
 1 MEDLDQSPLVSSSDSPPRPQPAFKYQFVREPEDEBEEEEEEEBEDBDEDLBELEVLERKPA
 DB 9; Length 373;
9 US-09-972-599A-6
14 US-10-060-036-71
15 US-10-10-267-502-429
16 US-10-37-213-9
16 US-10-37-213-9
16 US-10-37-213-9
17 US-10-10-653-23
18 US-10-810-653-20
18 US-09-893-348-20
18 US-09-893-348-18
18 US-10-63-218
18 US-09-893-348-25
18 US-09-893-348-25
18 US-09-893-348-25
18 US-09-893-348-21
18 US-09-893-348-21
18 US-09-893-348-21
18 US-09-893-348-21
18 US-09-893-348-21
18 US-09-893-348-21
18 US-09-893-348-21
18 US-09-893-348-21
18 US-09-893-348-21
18 US-09-893-348-21
18 US-09-893-348-21
18 US-09-893-348-21
18 US-09-893-348-21
18 US-09-893-348-21
18 US-09-893-348-21
18 US-09-893-348-21
18 US-09-893-348-21
18 US-09-893-348-21
18 US-09-893-348-21
18 US-09-893-348-21
18 US-09-893-348-21
18 US-09-893-348-21
18 US-09-893-348-21
18 US-09-893-348-21
18 US-09-893-348-21
18 US-09-893-348-21
18 US-09-893-348-21
18 US-09-893-348-21
18 US-09-893-348-21
18 US-09-893-348-21
 99.1%; Score 1833.8; DB 96.5%; Pred. No. 9.1e-56;
 0; Mismatches
 APPLICANT: MICHALOVICH, DAVID
APPLICANT: MICHALOVICH, DAVID
TITLE OF INVENTION: NOVEL COMPOUNDS
FILE REFERENCE: GP-30165-C1
CURRENT FILING DATE: 2001-02-21
FRIOR APPLICATION NUMBER: U.K. 9916898.1
PRIOR APPLICATION NUMBER: U.K. 9916898.1
PRIOR FILING DATE: 1999-07-19
PRIOR FILING DATE: 1998-07-22
PRIOR FILING DATE: 1998-07-22
PRIOR FILING DATE: 1999-07-22
NUMBER OF SEQ ID NOS: 6
SEQ ID NO 6
SEQ ID NO 6
SEQ ID NO 6
 ALIGNMENTS
 ; Sequence 6, Application US/09789386; Patent No. US20020010324A1; GENERAL INFORMATION:
 Best Local Similarity 96.5
Matches 360; Conservative
 ORGANISM: HOMO SAPIENS
 Similarity
 1756.9
1756.9
1756.9
1756.9
1756.9
1756.9
1756.9
1756.3
1756.3
1756.3
1756.3
1756.3
1756.3
1756.3
1756.3
1756.3
1756.3
1756.3
1756.3
1756.3
1756.3
1756.3
1756.3
1756.3
1756.3
1756.3
1756.3
1756.3
1756.3
1756.3
1756.3
1756.3
1756.3
1756.3
1756.3
1756.3
1756.3
1756.3
1756.3
1756.3
1756.3
1756.3
1756.3
1756.3
1756.3
1756.3
1756.3
1756.3
1756.3
1756.3
1756.3
1756.3
1756.3
1756.3
1756.3
1756.3
1756.3
1756.3
1756.3
1756.3
1756.3
1756.3
1756.3
1756.3
1756.3
1756.3
1756.3
1756.3
1756.3
1756.3
1756.3
1756.3
1756.3
1756.3
1756.3
1756.3
1756.3
1756.3
1756.3
1756.3
1756.3
1756.3
1756.3
1756.3
1756.3
1756.3
1756.3
1756.3
1756.3
1756.3
1756.3
1756.3
1756.3
1756.3
1756.3
1756.3
1756.3
1756.3
1756.3
1756.3
1756.3
1756.3
1756.3
1756.3
1756.3
1756.3
1756.3
1756.3
1756.3
1756.3
1756.3
1756.3
1756.3
1756.3
1756.3
1756.3
1756.3
1756.3
1756.3
1756.3
1756.3
1756.3
1756.3
1756.3
1756.3
1756.3
1756.3
1756.3
1756.3
1756.3
1756.3
1756.3
1756.3
1756.3
1756.3
1756.3
1756.3
1756.3
1756.3
1756.3
1756.3
1756.3
1756.3
1756.3
1756.3
1756.3
1756.3
1756.3
1756.3
1756.3
1756.3
1756.3
1756.3
1756.3
1756.3
1756.3
1756.3
1756.3
1756.3
1756.3
1756.3
1756.3
1756.3
1756.3
1756.3
1756.3
1756.3
1756.3
1756.3
1756.3
1756.3
1756.3
1756.3
1756.3
1756.3
1756.3
1756.3
1756.3
1756.3
1756.3
1756.3
1756.3
1756.3
1756.3
1756.3
1756.3
1756.3
1756.3
1756.3
1756.3
1756.3
1756.3
1756.3
1756.3
1756.3
1756.3
1756.3
1756.3
1756.3
1756.3
1756.3
1756.3
1756.3
1756.3
1756.3
1756.3
1756.3
1756.3
1756.3
1756.3
1756.3
1756.3
1756.3
1756.3
1756.3
1756.3
1756.3
1756.3
1756.3
1756.3
1756.3
1756.3
1756.3
1756.3
1756.3
1756.3
1756.3
1756.3
1756.3
1756.3
1756.3
1756.3
1756.3
1756.3
1756.3
1756.3
1756.3
1756.3
1756.3
1756.3
1756.3
1756.3
1756.3
1756.3
1756.3
1756.3
1756.3
1756.3
1756.3
1756.3
1756.3
1756.3
1756.3
1756.3
1756.3
1756.3
1756.3
1756.3
1756.3
1756.3
1756.3
1756.3
1756.3
1756.3
1756.3
1756.3
1756.3
1756.3
1756.3
1756.3
1756.3
1756.3
1756.3
1756.3
1756.3
1756.3
1756.3
1756.3
1756.3
1756.3
1756.3
1756.3
1756.3
1756.3
1756.3
1756.3
1756.3
1756.3
1756.3
1756.3
1756.3
1756.3
17
 LENGTH: 373
 08-09-789-386-6
 JS-09-789-386-6
 827.7
827.7
827.7
825.8
818.1
789.8
684.2
682.6
 TYPE: PRT
 Query Match
 유
 à
 ò
 Sequence 6, Appli
Sequence 4, Appli
Sequence 2, Appli
Sequence 6, Appli
Sequence 23, Appl
 (without alignments)
1271.831 Million cell updates/sec
 Sequence 6, Appli
Sequence 6, Appli
 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
 Sequence 72,
Sequence 8, Ay
Sequence 24,
Sequence 6, Ay
Sequence 4, Ay
 Sequence 24,
 VKDAMAKIQAKIPGLKRKAE 361
 Description
 June 23, 2005, 09:56:59 ; Search time 109.151 Seconds
 Published Applications AA:*

1: /cgn2_6/ptodata/1/pubpaa/USO7_PUBCOMB.pep:*
2: /cgn2_6/ptodata/1/pubpaa/PCT_MEW_PUB.pep:*
4: /cgn2_6/ptodata/1/pubpaa/USO6_NEW_PUB.pep:*
5: /cgn2_6/ptodata/1/pubpaa/USO6_NEW_PUB.pep:*
5: /cgn2_6/ptodata/1/pubpaa/USO6_NEW_PUB.pep:*
6: /cgn2_6/ptodata/1/pubpaa/USO8_NEW_PUB.pep:*
7: /cgn2_6/ptodata/1/pubpaa/USO8_NEW_PUB.pep:*
8: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*
9: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*
11: /cgn2_6/ptodata/1/pubpaa/USO9_PUBCOMB.pep:*
11: /cgn2_6/ptodata/1/pubpaa/USO9_PUBCOMB.pep:*
12: /cgn2_6/ptodata/1/pubpaa/USO9_PUBCOMB.pep:*
13: /cgn2_6/ptodata/1/pubpaa/USO9_PUBCOMB.pep:*
14: /cgn2_6/ptodata/1/pubpaa/USO9_PUBCOMB.pep:*
15: /cgn2_6/ptodata/1/pubpaa/USO9_PUBCOMB.pep:*
16: /cgn2_6/ptodata/1/pubpaa/USO9_PUBCOMB.pep:*
17: /cgn2_6/ptodata/1/pubpaa/USO9_PUBCOMB.pep:*
18: /cgn2_6/ptodata/1/pubpaa/USO9_PUBCOMB.pep:*
19: /cgn2_6/ptodata/1/pubpaa/USO9_PUBCOMB.pep:*
19: /cgn2_6/ptodata/1/pubpaa/USO9_PUBCOMB.pep:*
21: /cgn2_6/ptodata/1/pubpaa/USO9_PUBCOMB.pep:*
22: /cgn2_6/ptodata/1/pubpaa/USO9_PUBCOMB.pep:*
 5.1.6
Compugen Ltd.
 US-10-060-035-72

US-10-408-967-8

US-10-310-653-24

US-10-347-669-6

US-10-466-258-4

US-09-789-386-2

US-09-789-386-2

US-09-789-348-23
 Total number of hits satisfying chosen parameters:
 US-09-789-386-6
US-09-765-205-6
US-09-893-348-24
 1717557 seqs, 384547976 residues
 GenCore version
Copyright (c) 1993 - 2005
 SUMMARIES
 Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
 - protein search, using sw model
 BLOSUM62
Gapop 10.0 , Gapext 0.1
 US-09-830-972-29-FUSED
1850
1 MEDLDQSPLVSSSDSPPRPQ.
 Minimum DB seq length: 0
Maximum DB seq length: 2000000000
 DB
 Length
 373
1192
1192
1192
 Query
Match 1
 Title:
Perfect score:
 Scoring table:
 1833.8
1833.8
1833.8
1833.8
1833.8
1833.8
1833.8
1756.9
```

sequence 21, Appl Sequence 11, Appl Sequence 5, Appl 1 Sequence 430, App Sequence 432, App Sequence 93, Appl Sequence 93, Appl Sequence 6, Appl 1 Sequence 2892, Appl 2 Sequence 2892, Appl 2

Sequence 8, Appl:

Sequence

9

1; Indels

4 5 9 6 5 1

Result М В

Sequence 25, Appl Sequence 1, Appl Sequence 25, Appl Sequence 9, Appl Sequence 467, App Sequence 21, Appl Sequence 21, Appl

Sequence 20, Appl Sequence 10, Appl Sequence 18, Appl Sequence 10, Appl Sequence 10, Appl Sequence 431, App Sequence 25, Appl Sequence 25, Appl

Sequence 9, Al Sequence 23, 7 Sequence 7, Al

Sequence 164,

(1

```
APPLICANT: COHEN, ITULE R.
APPLICANT: COHEN, ITULE R.
APPLICANT: BESERWAN, Pierre
APPLICANT: BESERWAN, Pierre
APPLICANT: MOALEM, Gila
TITLE OF INVENTION: ACTIVATED T-CELLS, NERVOUS SYSTEM-SPECIFIC ANTIGENS AND THEIR US)
FILE REPERRENCE: EIS-SCHWARTES-2A
CURRENT APPLICATION NUMBER: US/09/893,348
CURRENT APPLICATION NUMBER: US 09/314,161
PRIOR APPLICATION NUMBER: US 09/314,161
PRIOR PILING DATE: 1998-12-22
PRIOR APPLICATION NUMBER: US 09/218,277
PRIOR APPLICATION NUMBER: ET/V898/14715
PRIOR PILING DATE: 1998-07-21
PRIOR APPLICATION NUMBER: IL 124500
PRIOR APPLICATION NUMBER: IL 124500
PRIOR APPLICATION NUMBER: IL 124500
PRIOR SEQ ID NOS: 29
NUMBER OF SEQ ID NOS: 29
 61 AGLSAAPVPTAPAAGAPLMDFGNDFVPPAPRGPLPAAPPVAPERQPSWDSSTVSSTVPAP 120
 241 VIQAIQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNCTIKELRRLFLVVDDLVDSL 300
 289 KFAVLMWVFTYVGALFNGLTLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAK 348
 121 SPLSAAAVSPSKLPEDDEPPARPPPPPASVSPQAEPVWTPPAPAPAAPPSTPAAPKRRG 180
 181 SSGSVVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKG
 1 MEDILOQSPLVSSSDSPPRPQPAFKYQFVREPEDEEEEEEEEEEEEEEEEEEEEEEEEFEVLERKPA
 61 AGLSAAPVPTAPAAGAPLMDFGNDFVPPAPRGPLPAAPPVAPERQPSWDPSPVSSTVPAP
 174 -----WDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKG
 229 VIQAIQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNCTIKELRRIFLVDDLVDSL
 1 MEDLDQSPLVSSSDSPPRPQPAFKYQFVREPEDEBEEEEEEEEDEDEDLEELEVLERKPA
 121 SPLSAAAVSPSKLPEDDEPPARPPPPASVSPQAEPVWTPPAPAPAPAPSTS-----
 12;
 DB 9; Length 373;
 1; Indels
 Score 1833.8; DB 5
Pred. No. 9.1e-56;
0; Mismatches 1;
 Michal
 Sequence 72, Application US/10060036; Publication No. US20030073144A1
GENERAL INFORMATION: APPLICANT: Benson, Darin R.
 Sequence 24, Application US/09893348
Patent No. US20020072493A1
GENERAL INFORMATION:
APPLICANT: EISENBACH-SCHWARTZ, Miche
 vuery Match 99.1%;
Best Local Similarity 96.5%;
Matches 360; Conservative (
361 IQAKIPGLKRKAE 373
 349 IQAKIPGLKRKAE 361
 ORGANISM: Homo sapiens
 US-09-893-348-24
 361
 셤
 g
 셤
 ò
 g
 ò
 g
 ò
 ઠ
 g
 ò
 d
 ઠે
 AGLSAAPVPTAPAAGAPLMDFGNDFVPPAPRGPLPAAPPVAPERQPSWDFSPVSSTVPAP 120
 288
61 AGLSAAPVPTAPAAGAPLMDFGNDFVPPAPRGPLPAAPPVAPBRQPSWDPSPVSSTVPAP 120
 228
 VIQAIQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDSL 288
 300
 61 AGLSAAPVPTAPAAGAPLMDFGNDFVPPAPRGPLPAAPPVAPERQPSWDPSPVSSTVPAP 120
 174 -----VVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKG 228
 300
 KFAVLMWVFTYVGALFNGLTLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAK 348
 SPLSAAAVSPSKLPEDDEPPARPPPPASVSPQAEPVWTPPAPAPAPPSTS----- 173
 9
 9
 Sequence 6, Application US/09765205;
Patent No. US20020034800A1
GENERAL INFORMATION:
APPLICANT: Cao, Li
TITLE OF INVENTION: BONE MARROW SECRETED PROTEINS AND POLYNUCLEOTIDES
FILE REPRESENCE: 1458.004/200130.449
CURRENT FILING DATE: 2001-01-17
PRIOR PAPLICATION NUMBER: US/09/765,205
CURRENT FILING DATE: 1998-12-16
NUMBER OF SEQ ID NOSHE: 1998-12-16
NUMBER OF SEQ ID NOS: 46
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 6
LENGTH: 373
 SPLSAAAVSPSKLPEDDEPPARPPPPASVSPQAEPVWTPPAPAPAAPPSTS-----
 174 -----WVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKG
 181 SSGSVVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKG
 241 VIQAIQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDSL
 1 MEDLDQSPLVSSSDSPPRPQPAFKYQFVREPEDBEBEBEBEBEBDEDLBBLEVLBRKPA
 1 MEDLIDQSPLVSSSDSPPRPQPAFKYQFVREPEDEEEEEEEEEEDEDEDLEELEVLERKPA
 181 SSGSVVVDLLYWRDIKKTGVVFGASLFLLSLTVFSIVSVTAYIALALLSVTISFRIYKG
 VIQAIQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNCTIKELRRIFLVDDLVDSL
 241 VIQAIQKSDEGHPFRAYLBSEVAISBELVQKYSNSALGHVNCTIKELRRLFLVDDLVDSL
 Gaps
 12;
 Query Match 99.1%; Score 1833.8; DB 9; Length 373; Best Local Similarity 96.5%; Pred. No. 9.1e-56; Matches 360; Conservative 0; Mismatches 1; Indels 12;
 IQAKIPGLKRKAE 361
 361 IQAKIPGLKRKAE 373
 IQAKIPGLKRKAE 361
 ORGANISM: human
 RESULT 2
US-09-765-205-6
 ; ORGANISM: hu
US-09-765-205-6
 229
 349
 121
 61
 121
 229
 349
 289
 셤
 g
 유
 g
 g
 g
 ò
 g
 ò
 ò
 ò
 ò
 셤
 ò
 ð
 ð
 셤
 ò
 ò
 ઠે
```

Gaps

```
APPLICANT: ELEABRANGE STATEMENT APPLICANT: BESERMAN, PIETE APPLICANT: BESERMAN, PIETE APPLICANT: BESERMAN, PIETE APPLICANT: BESERMAN, PIETE APPLICANT: MOSONEGO, Alon APPLICANT: MOSONEGO, Alon APPLICANT: MOALEW, Gila CHENGER STATE APPLICANT: MOALEW, Gila CURRENT BOLICATION NUMBER: US/09/893,348

FILE REPERBUCE: ELS-SCHWARTZ-2A

CURRENT APPLICATION NUMBER: US/09/893,348

PRIOR APPLICATION NUMBER: US/09/893,348

PRIOR APPLICATION NUMBER: US/09/893,161

PRIOR FILING DATE: 1999-05-19

PRIOR FILING DATE: 1998-05-22

PRIOR FILING DATE: 1998-05-22

PRIOR FILING DATE: 1998-07-21

PRIOR FILING DATE: 1998-05-19

PRIOR FILING DATE: 1998-05-19

PRIOR FILING DATE: 1998-05-19

NUMBER OF SEQ ID NOS: 29

SOFTWARKE: PATENTIN VERSION 3.1
 ä
 61 AGLSAAPVPTAPAAGAPLMDFGNDFVPPAPRGPLPAAPPVAPERQPSWDPSPVSSTVPAP 120
 121 SPLSAAAVSPSKLPEDDEPPARPPPPPASVSPQAEPVWTPPAPAAPAAPSTPAAPKRG 180
 181 SSGSVVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKG 240
 121 SPLSAAAVSPSKLPEDDEPPARPPPPASVSPQAEPVWTPPAPAAPPASTS----- 173
 174 -----VVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKG 228
 241 VIQAIQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDSL 300
 301 KFAVLMMYFTYVGALFNGLTLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAK 360
 61 AGLSAAPVPTAPAAGAPLMDFGNDFVPPAPRGPLPAAPPVAPERQPSWDPSPVSSTVPAP 120
 61 AGLSAAPVPTAPAAGAPLMDFGNDFVPPAPRGPLPAAPPVAPERQPSWDPSPVSSTVPAP 120
 VIQAIQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDSL 288
 KFAVLAMVFTYVGALFNGLTLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAK 348
 1 MEDLDQSPLVSSSDSPPRPQPAFKYQFVREPEDEEEEEEEEEEEDEDLEELEVLERKPA 60
 1 MEDLIDQSPLVSSSDSPPRPQPAFKYQFVREPEDEEEEEEEEEEEEEEEDEDEDLEELEVLERKEPA 60
 1 MEDLDQSPLVSSSDSPPRPQPAFKYQFVREPEDEEEEEEEEEEEDEDLEELEEVLERKPA
 Gaps
 12;
 12;
 DB 16; Length 373;
 1; Indels
 IndelB
 99.1%; Score 1833.8; DB : 96.5%; Pred. No. 9.1e-56; iive 0; Mismatches 1.
 Mismatches
 APPLICANT: EISENBACH-SCHWARTZ, Michal
 ; Sequence 24, Application US/10810653; Publication No. US20040253218A1; GENERAL INFORMATION:
 ö
 IQAKIPGLKRKAE 361
 361 IQAKIPGLKRKAE 373
 Matches 360; Conservative
 Query Match
Best Local Similarity 96.5
Matches 360; Conservative
 US-10-810-653-24
 349
 229
 289
 g
 g
 ઠે
 Š
 ð
 a
 ઠે
 g
 셤
 ò
 셤
 В
 ò
 ò
 ઠે
 ઠે
 COURTENT INFORMATION:
APPLICANT: Yan, Ridiang
APPLICANT: Yan, Ridiang
APPLICANT: Lu, Yifeng
TITLE OF INVENTION: Compositions and Methods of Treating Alzheimer's Disease
FILE REPERENCE: 00929
TITLE OF INVENTION: Compositions and Methods of Treating Alzheimer's Disease
CURRENT APPLICATION NUMBER: US/10/408,967
CURRENT FILING DATE: 2003-04-08
NUMBER OF SEQ ID NOS: 9
SEOTWARE: PatentIn version 3.1
SEQ ID NO 8
LENGTH: 373
 181 SSGSVVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKG 240
 120
 61 AGLSAAPVPTAPAAGAPLMDFGNDFVPPAPRGPLPAAPPVAPERQPSWDPSPVSSTVPAP 120
 173
 228
 VIQAIQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDSL 288
 VIQAIQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDSL 300
 KFAVLAMWVFTYVGALFNGLTLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAK 348
 9
 9
 1 MEDLDQSPLVSSSDSPPRPQPAFKYQFVREPEDEBEEEEEEEBDEDLEELEVLERKPA
 AGLSAAPVPTAPAAGAPLMDFGNDFVPPAPRGPLPAAPPVAPERQPSWDPSPVSSTVPAP
 1 MEDLIDQSPLVSSSDSPPRPQPAFKYQFVREPEDEEEEEEEEEEDEDEDLEELEVLERKPA
 SPLSAAAVSPSKLPEDDEPPARPPPPRASVSPQAEPVWTPPAPAPAAPPSTS-----
 ----VVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKG
 Query Match 99.1%; Score 1833.8; DB 14; Length 373; Best Local Similarity 96.5%; Pred. No. 9.1e-56; Matches 360; Conservative 0; Mismatches 1; Indels 12; Gaps
APPLICANT: Kalos, Michael D.
APPLICANT: Lodes, Michael J.
APPLICANT: Lodes, Michael J.
APPLICANT: Hepler, William T.
APPLICANT: Hepler, William T.
APPLICANT: Hopler, William T.
APPLICANT: Jiang, Yuqiu
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF PANCREATIC CANCER
FILE REFERENCE: 210121.566
CURRENT APPLICATION NUMBER: US/10/060,036
CURRENT APPLICATION NUMBER: US/10/060,036
NUMBER OF SEQ ID NOS: 4560
SOFTWARR: FastSEQ for Windows Version 4.0
 Score 1833.8; DB 15; Length 373;
Pred. No. 9.1e-56;
 99.1%;
96.5%;
 IQAKIPGLKRKAE 373
 349 IQAKIPGLKRKAE 361
 TYPE: PRT
CORGANISM: Homo sapiens
US-10-060-036-72
 TYPE: PRT
CRGANISM: Homo sapiens
US-10-408-967-8
 Query Match
Best Local Similarity
 RESULT 5
US-10-408-967-8
 LENGTH: 373
 241
 61
 121
 121
 174
 229
 289
 301
 361
```

셤 ò g ઠ 유 ò g ઠે

g

ò

g ઠે

ઠે

셤

ò

g ò 셤 ò g ò 원

ò

```
240
 120
 121 SPLSAAAVSPSKLPQDDEPPARPPPPPASVSPQAEPVWTPPAAPAAPPSTPAAPKRG 180
 VIQAIQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDSL 288
 KFAVLMWVFTYVGALFNGLTLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAK 348
 9
 9
 SSGSVVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKG
 AGLSAAPVPTAPAAGAPLMDFGNDFVPPAPRGPLPAAPPVAPERQPSWDPSPVSSTVPAP
 ----VVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKG
 MEDILDOSPLVSSSDSPPRPQPAFKYQFVREPEDEBEBEBEBEBEBEBDBDLBELEVLERKPA
 1 MEDLDQSPLVSSSDSPPRPQPAFKYQFVREPEDEEEEEEEEEDEDEDLEELEVLERKPA
 SPLSAAAVSPSKLPEDDEPPARPPPPASVSPQAEPVWTPPAPAPAPAPSTS-----
 Gaps
 12;
 Length 373;
 Indels
 DB 16;
 Score 1825.8; DB 16
Pred. No. 1.7e-55;
1; Mismatches 2;
 GROWN OF A SEQUENCE OF A SEQUE
 APPLICANT: GLAXO GROUP LIMITED
TITLE OF INVENTION: ASSAY
FILLE REFERENCE: P80966 GCW
CURRENT APPLICATION NUMBER: US/10/466,258
CURRENT FILING DATE: 2003-07-15
NUMBER OF SEQ ID NOS: 13
SOFTWARE: Patentin version 3.0
 Sequence 4, Application US/10466258
Publication No. US20040132096A1
GENERAL INFORMATION:
 98.7%;
96.0%;
 361 IQAKIPGLKRKAE 373
 IQAKIPGLKRKAE 361
 361 IQAKIPGLKRKAE 373
 Best Local Similarity 96.0
Matches 358; Conservative
 TYPE: PRT
ORGANISM: Homo sapiens
 LENGTH: 373
 US-10-466-258-4
 US-09-789-386-2
 349
 61
 121
 174
 181
 241
 289
 301
 229
 Query Match
 셤
 ઠ
 셤
 ò
 qq
 ò
 ď
 ò
 Db
 ò
 qq
 Š
 g
 ò
 ij
 120
 300
 121 SPLSAAAVSPSKLPEDDEPPARPPPPPASVSPQAEPVWTPPAPAPAPAPAPAPAPKRRG 180
 181 SSGSVVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKG 240
 241 VIQAIQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNCTIKELRRLFLVVDDLVDSL 300
 301 KFAVLAMWFTYVGALFNGLTLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAK 360
 61 AGLSAAPVPTAPAAGAPLMDFGNDFVPPAPRGPLPAAPPVAPERQPSWDPSPVSSTVPAP 120
 173
 240
 301 KFAVLMMVFTYVGALFNGLTLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAK 360
61 AGLSAAPVPTAPAAGAPLMDFGNDFVPPAPRGPLPAAPPVAPERQPSWDPSPVSSTVPAP 120
 KFAVLMWVFTYVGALFNGLTLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAK 348
 174 -----VVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKG 228
 VIQAIQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDSL 288
 KFAVLMWVFTYVGALFNGLTLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAK 348
 1 MEDLDQSPLVSSSDSPPRPQPAFKYQFVREPEDEEEEEEEEEDEDEDLEELEVLERKPA 60
 181 SSGSVVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKG
 174 -----WUDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKG
 VIQAIQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNCTIKELRRFLFLVDDLVDSL
 61 AGLSAAPVPTAPAAGAPLMDFGNDFVPPAPRGPLPAAPPVAPERQPSWDPSPVSSTVPAP
 241 VIQAIQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDSL
 1 MEDLDQSPLVSSSDSPPRPQPAFKYQFVREPEDEEEEEEEEEEDEDEDLEELEVLERKPA
 121 SPLSAAAVSPSKLPEDDEPPARPPPPASVSPQAEPVWTPPAAPAPAPSTS-----
 Gaps
 APPLICANT: Cao, Li.
TITLE OF INVENTION: BONE MARROW SECRETED PROTEINS AND POLYNUCLEOTIDES FILE REFERENCE: 1458.004/200130.449
FILE REFERENCE: 1458.004/200130.449
CURRENT APPLICATION NUMBER: US/10/347,669
CURRENT FILING DATE: 2003-01-16
PRIOR APPLICATION NUMBER: US/09/212,440
PRIOR FILING DATE: 1998-12-16
NUMBER OF SEQ ID NOS: 46
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 6
LENGTH: 373
 SPLSAAAVSPSKLPEDDEPPARPPPPPASVSPQAEPVWTPPAPAAPPPSTS--
 Score 1833.8; DB 17; Length 373;
Pred. No. 9.1e-56;
0; Mismatches 1; Indels 12;
 Sequence 6, Application US/10347669 Publication No. US20050084850A1 GENERAL INFORMATION:
 Query Match
Best Local Similarity 96.5%;
Matches 360; Conservative
 361 IQAKIPGLKRKAE 373
 349 IQAKIPGLKRKAE 361
 IQAKIPGLKRKAE 361
 ; TYPE: PRT
; ORGANISM: human
US-10-347-669-6
 US-10-347-669-6
 289
 229
 229
 289
 121
```

g

δ В ò g ò 임 ò

ద à 임

1020

249

189

1140

```
TITLE OF INVENTION:

TITLE OF INVENTION:

NO. US20020012965Alo Receptor-Mediated Blockade of Axonal Growt

TITLE OF INVENTION:

NO. US20020012965Alo Receptor-Mediated Blockade of Axonal Growt

PILE REPERENCE:

44574-5073-US

CURRENT APPLICATION NUMBER: US 60/175,107

PRIOR APPLICATION NUMBER: US 60/207,366

PRIOR PILING DATE: 2000-01-12

PRIOR APPLICATION NUMBER: US 60/207,366

PRIOR APPLICATION NUMBER: US 60/236,378

PRIOR FILING DATE: 2000-09-29
 VAISEELVOKYSNSALGHVNCTIKELRRLFLVDDLVDSLKRAVLMWVFTYVGALFNGLTL 309
 61 AGLSAAPVPTAPAAGAPLMDFGNDFVPPAPRGPLPAAPPVAPERQPSWDPSFVSTVPAP 120
 241 LSAASFKEHEYLGNLSTVLPTEGTLQENVSEASKEVSEKAKTLLIDRDLTEFSELEYSEM 300
 301 GSSFSVSPKAESAVIVANPREEIIVKNKDEEEKLVSNNILHNQQELPTALTKLVKEDEVV 360
 361 SSEKAKDSFNEKRVAVEAPMREEYADFKPFERVWEVKDSKEDSDMLAAGGKIESNLESKV 420
 1 MEDLDQSPLVSSSDSPPRPQPAFKYQFVREPEDEEEEEEEEEEBDBDEDLBELEVLERKPA 60
 QAEIESIVKPKVLVKEAEKKLPSDTEKEDRSPSAIFSAELSKTSVVDLLYWRDIKKTGVV
 FGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQAIQKSDEGHPFRAYLESE
 61 AGLSAAPVPTAPAAGAPLMDFGNDFVPPAPRGPLPAAPPVAPERQPSWDPSPVSSTVPAP
 MEDLDQSPLVSSSDSPPRPQPAFKYQFVREPEDEEEEEEEEEEDEDLEELEVLERKPA
 181 SSGSVDETLFALPAASEPVIRSSAENMDLKEQPGNTISAGQEDFPSVLLETAASLPSLSP
 Indels 831; Gaps
 Length 1192;
 121 SPLSAAAVSPSKLPEDDEPPARPPPPPASVSPQAEPVWTPPAPAPAPPS---
 3;
,.2e-52;
0;
 DB 9;
 Score 1756.9;
Pred. No. 3.2e-
0; Mismatches
 ; Sequence 6, Application US/09758140; Patent No. US20020012965A1; GENERAL INFORMATION:
 Query Match
Best Local Similarity 30.3%;
Matches 361; Conservative
 PatentIn Ver. 2.1
 ORGANISM: Homo sapiens
 NUMBER OF SEQ ID NOS:
SOFTWARE: PatentIn Ve
 US-09-758-140-6
 US-09-758-140-6
 250
 1141
 961
 310
 172
 190
 SEQ ID NO 6
 172
 172
 TYPE: PRT
 172
 172
 유
 ò
 셤
 ઠે
 셤
 셤
 δ
 ₽
 셤
 g
 g
 8
 셤
 ò
 g
 ઠે
 셤
 ŝ
 δ
 ò
 ઠે
 ï
 AGLSAAPVPTAPAAGAPLMDFGNDFVPPAPRGPLPAAPPVAPERQPSWDPSPVSSTVPAP 120
 SPLSAAAVSPSKLPEDDEPPARPPPPPASVSPQAEPVWTPPAPAPAPAPS----- 171
 171
 171
 241 LSAASFKEHEYLGNLSTVLPTEGTLQENVSEASKEVSEKAKTLLIDRDLTEFSELEYSEM 300
 301 GSSFSVSPKAESAVIVANPREEIIVKNKDEEEKLVSNNILHNQQELPTALTKLVKEDEVV 360
 171
 171
 540
 840
 900
 SSEKAKDSFNEKRVAVEAPMREEYADFKPFERVWEVKDSKEDSDMLAAGGKIESNLESKV 420
 421 DKKCPADSLEQTNHEKDSESSNDDTSFPSTPEGIKDRPGAYITCAPFNPAATESIATNIF 480
 171
 171
 541 EVVANMPEGLIPDLVQEACESELNEVIGTKIAYETKMDLVQISEVMQESLYPAAQLCPSF 600
 171
 780
 901 ANAPDGAGSLPCTELPHDLSLKNIQPKVEEKISFSDDFSKNGSATSKVLLLPPDVSALAT 960
 661 EAMSVSLKKVSGIKEEIKEPENINAALQETEAPYISIACDLIKETKLSAEPAPDFSDYSE 720
 1 MEDLDQSPLVSSSDSPPRPQPAFKYQFVREPEDEEEEEEEEEEDEDEDLEELEVLERKPA
 181 SSGSVDETLFALPAASEPVIRSSAENMDLKEQPGNTISAGQEDFPSVLLETAASLPSLSP
 PLIGDPTSENKTDEKKIEEKKAQIVTEKNTSTKTSNPFLVAAQDSETDYVTTDNLTKVTE
 601 EESEATPSPVLPDIVMEAPLNSAVPSAGASVIQPSSSPLEASSVNYESIKHEPENPPPYE
 721 MAKVEQPVPDHSELVEDSSPDSEPVDLFSDDSIPDVPQKQDETVMLVKESLTETSFESMI
 781 EYENKEKLSALPPEGGKPYLESFKLSLDNTKDTLLPDEVSTLSKKEKIPLQMEELSTAVY
 841 SNDDLFISKEAQIRETETFSDSSPIEIIDEFPTLISSKTDSFSKLAREYTDLEVSHKSEI
 Score 1756.9; DB 9; Length 1192;
Pred. No. 3.2e-52;
0; Mismatches 0; Indels 831; Gaps
 95.0%;
30.3%;
 Best Local Similarity 30.3
Matches 361; Conservative
 LENGTH: 1192
TYPE: PRT
ORGANISM: HOMO SAPIENS
 ; ORGANISM: HC
US-09-789-386-2
 61
 361
SEQ ID NO 2
 121
 121
 481
 172
 172
 172
 172
 172
 172
 172
 172
 172
 172
 172
 172
 172
 Query Match
 ઠે
 셤
 ઠે
 셤
 ઠે
 D
 ò
 g
 셤
 셤
 ઠે
 셤
 ò
 ద
 ò
 셤
 ઠે
 염
 ò
 셤
 ઠે
 a
 g
 ò
 요
 g
 ઠે
 ઠે
 셤
 ઠે
 ò
 ò
```

ä

120

171

| PRIOR FILING DATE: 1998-07-21<br>PRIOR APPLICATION NUMBER: IL 124500 | SEQ ID NOS: 29                                                          | racentin version 3<br>23 | T                                                                       | COANIENT: HOURD BADIETIB<br>-893-348-23 | Mat                                                                     | LOCAI SIMIIATILY 30.34; FIEG. NO. 3.2<br>Es 361; Conservative 0; Mismatches | 1 MEDLDQSPLVSSSDSPPRPQPAFKYQFVREPEDEEEEEEEEEEEDEDEDLEELEVLERKPA 60     | 1 MEDLDQSPLVSSSDSPPRPQPAFKYQFVREPEDEEEEEEEEEEEEDEDEDLEELVLERKPA 60 | 61 AGISAAPVPTAPAAGAPLMDFGNDFVPPARGPLPAAPPVAPERQPSWDSSPVSSTVPAP 120      | 61 AGLSAAPVETAPAAGAPLMDFGNDFVPPAPRGPLPAAPPVAPERQPSWDPSPVSSTVPAP 120 | 121 SPLSAAAVSPSKLPEDDEPPARPPPPASVSPQAEPVWTPPAPAPAPPS 171                |            | 172 171                                                                 | 181 SSGSVDETLFALPAASEPVIRSSAENMDLKEQPGNTISAGGEDFPSVLLETAASLPSLSP 240 | 172 171                                                                 | 241 LSAASFKEHEYLGNLSTVLPTEGTLQENVSEASKEVSEKAKTLLIDRDLTEFSELEYSEM 300 | 172 171                                                                 | 301 GSSFSVSPKAESAVIVANPREEIIVKNKDEEEKLVSNNILHNQQELPTALTKLVKEDEVV 360 | 172 171                                                                  | SSEKAKDSFNEKRVAVEAPMREEYADFKPFBRVWEVKDSKEDSDMLAAGGKIESNLESKV    | 172 171                                                                   | DKKCFADSLEQTNHEKDSESSNDDTSFPSTPEGIKDRPGAYITCAPFNPAATESIATNIF | 172                                                                       | 481 PLLGDPTSENKTDEKKIEEKKAQIVTEKNTSTKTSNPFLVAAQDSETDYVTTDNLTKVTE 540 | 172 171                                                           | 541 EVVANMPEGLTPDLVQEACESELNEVTGTKIAYETKMDLVQTSEVMQESLYPAAQLCPSF 600 | 172 171                                                                 | 601 EESEATPSPVLPDIVMEAPLNSAVPSAGASVIQPSSSPLEASSVNYESIKHEPENPPPYE 660 | 172 171                                                     | 661 EAMSVSLKKVSGIKEEIKEPENINAALQETEAPYISIACDLIKETKLSAEPAPDFSDYSE 720 | 172 171                                                                                                                    | 721 MAKVEQPVPDHSELVEDSSPDSEPVDLFSDDSIPDVPQKQDETVMLVKESLTETSFESMI 780                                  | 172 171                                                                   | 781 EYENKEKLSALPPEGGKPYLESFKLSLDNTKDTLLPDEVSTLSKKEKIPLQMEELSTAVY 840 | 172 171                                  |
|----------------------------------------------------------------------|-------------------------------------------------------------------------|--------------------------|-------------------------------------------------------------------------|-----------------------------------------|-------------------------------------------------------------------------|-----------------------------------------------------------------------------|------------------------------------------------------------------------|--------------------------------------------------------------------|-------------------------------------------------------------------------|---------------------------------------------------------------------|-------------------------------------------------------------------------|------------|-------------------------------------------------------------------------|----------------------------------------------------------------------|-------------------------------------------------------------------------|----------------------------------------------------------------------|-------------------------------------------------------------------------|----------------------------------------------------------------------|--------------------------------------------------------------------------|-----------------------------------------------------------------|---------------------------------------------------------------------------|--------------------------------------------------------------|---------------------------------------------------------------------------|----------------------------------------------------------------------|-------------------------------------------------------------------|----------------------------------------------------------------------|-------------------------------------------------------------------------|----------------------------------------------------------------------|-------------------------------------------------------------|----------------------------------------------------------------------|----------------------------------------------------------------------------------------------------------------------------|-------------------------------------------------------------------------------------------------------|---------------------------------------------------------------------------|----------------------------------------------------------------------|------------------------------------------|
| ; ;                                                                  | Y N                                                                     | SEO.                     |                                                                         | 60-SN                                   | Query                                                                   | Mat                                                                         | ò                                                                      | ΩP                                                                 | ò                                                                       | qq                                                                  | λõ                                                                      | qq         | ò                                                                       | qu                                                                   | ò                                                                       | qq                                                                   | δ                                                                       | QO                                                                   | ò                                                                        | qq                                                              | ò                                                                         | Ωp                                                           | δò                                                                        | Ор                                                                   | ò                                                                 | Ωp                                                                   | ò                                                                       | qq                                                                   | δ                                                           | qq                                                                   | ò                                                                                                                          | qq                                                                                                    | λ                                                                         | ф                                                                    | λ                                        |
| Qy 172 171                                                           | Db 421 DKKCFADSLEQTNHEKDSESSNDDTSFPSTPEGIKDRSGAYITCAPFNPAATESIATNIF 480 | Qy 172 171               | Db 481 PLLGDPTSENKTDEKKIEEKKAQIVTEKNTSTKTSNPFLVAAQDSETDYVTTDNLTKVTE 540 | Qy 172 171                              | Db 541 EVVANMPEGLTPDLVQEACESELNEVTGTKIAYETKMDLVQTSEVMQESLYPAAQLCPSF 600 | Оу 172 171                                                                  | Db 601 EESEATPSPVLPDIVMEAPLNSAVPSAGASVIQPSSSPLEASSVNYESIKHEPENPPYE 660 | Qy 172 171                                                         | Db 661 EAMSVSLKKVSGIKEEIKEPENINAALQETEAPYISIACDLIKETKLSAEPAPDFSDYSE 720 | Oy 172 171                                                          | Db 721 MAKVEQPVPDHSELVEDSSPDSEPVDLFSDDSIPDVPQKQDETVMLVKESLTETSFESMI 780 | Qy 172 171 | Db 781 EYENKEKLSALPPEGGKPYLESFKLSLDNTKDTLLPDEVSTLSKKEKIPLQMEELSTAVY 840 | Qy 172 171                                                           | Db 841 SNDDLFISKEAQIRETETFSDSSPIEIIDEFPTLISSKTDSFSKLAREYTDLEVSHKSEI 900 | Qy 172 171                                                           | Db 901 ANAPDGAGSLPCTELPHDLSLKNIQPKVEEKISFSDDFSKNGSATSKVLLLPPDVSALAT 960 | Qy 172TSVVDLLYWRDIKKTGVV 189                                         | Db 961 QAEIESIVKPKVLVKEAEKKLPSDTEKEDRSPSAIFSAELSKTSVVDLLYWRDIKKTGVV 1020 | 190 FGASLFLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQAIQKSDEGHPFRAYLESE | Db 1021 FGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQAIQKSDEGHPFRAYLESE 1080 | 250 VAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDSLKFAVLMWVFTYVGA    | Db 1081 VAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDSLKFAVLMMVFTYVGALFNGLTL 1140 | Qy 310 LILALISLESUPVIYERHQAQIDHYLGLANKNYKDAMAKIQAKIPGLKRKAE 361      | Db 1141 LILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAKIPGLKRKAE 1192 | 11 - 110000                                                          | ABSOLA 21<br>2.09-09-33-348-23<br>. 6.00-000-01 Ammliantian HG/00000000 | 93A1                                                                 | , APPLICANT: EISENBRITZ, Michal , ADPLICANT: COURM IT TO BE | APPLICANT: BESERMAN PIETE ADPLICANT: MCCNAFC Alor                    | ברבות<br>רביה הימיהיות הימיהים מותמים מותמים מותמים הימיהים המיהים מותמים מותמים מותמים מותמים מותמים מותמים מותמים מותמים | CCIIVATED I-CELES, NEKVOOS SISIEM-SFECIFIC ANIIGENS AND INEIK<br>ICHWARTEZ 2A<br>IMPED IIS/04/893 348 | CURRENT FILLING DATE: 2001-06-28 PRIOR APPLICATION WIMMER: 130 09/314 161 | PRIOR FILING DATE: 1999-05-19                                        | FILING DATE: 1998-12 APPLICATION NUMBER: |

|                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                | _                               |                                                                      |
|--------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|---------------------------------|----------------------------------------------------------------------|
|                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                | SEI 900 Db 241                  | LSAASFKEHEYLGNLSTVLPTEGTLQENVSEASKEVSEKAKTLLIDRDLTEFSELEYSEM 300     |
| Qy 172                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         | 171 Qy 172                      | 171                                                                  |
| Db 901 ANAPDGAGSLPCTELPHDLSLKNIQPKVEEKISFSDDFSKNGSATSKVLLLPPDVSALAT                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            | AT 960 Db 301                   | GSSFSVSPKAESAVIVANPREEIIVKNKDEEEKLVSNNILHNQQELPTALTKLVKEDEVV 360     |
| Qy 172TSVVDLLYWRDIKKTGVV                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       | 3VV 189 Qy 172                  | 171                                                                  |
| Db 961 QAEIESIVKPKVLVKEAEKKLPSDTEKEDRSPSAIFSAELSKTSVVDLLYWRDIKKTGVV                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            | 361 Db 361                      | SSEKAKDSFNEKRVAVEAPMREEYADFKPFERVWEVKDSKEDSDMLAAGGKIESNLESKV 420     |
| Qy 190 FGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQAIQKSDEGHPFRAYLESE                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            | SSE 249 Qy 172                  | 171                                                                  |
| Db 1021 FGASLFILLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQAIQKSDEGHPFRAYLES                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            | 3SE 1080 Db 421                 | DKKCPADSLEQTNHEKDSESSNDDTSFPSTPEGIKDRSGAYITCAPFNPAATESIATNIF 480     |
| Qy 250 VAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDSLKFAVLMMVFTYVGALFNGLTL                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            | 172 309 QY 172                  | 171                                                                  |
| DD 1081 VAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDSLKFAVLMWVFTYVGALFNGLT                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            | IL 1140 Db 481                  | PLLGDPTSENKTDEKKIEEKKAQIVTEKNTSTKTSNPFLVAAQDSETDYVTTDNLTKVTE 540     |
| Qy 310 LILALISLFSVPVIYERHQAQIDHYLGLANKOVKDAMAKIQAKIPGLKRKAE 361                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                | Oy 172                          | 171                                                                  |
| Db 1141 LILALISUPSVIYERHQAQIDHYLGLANKNVKDAMAKIQAKIPGLKRKAE 1192                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                | Db 541                          | EVVANMPEGLIPDLVQEACESELNEVTGTKIAYETKMDLVQTSEVMQESLYPAAQLCPSF 600     |
| PECITI 12                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      | Qy 172                          | 171                                                                  |
| US-09-972-599A-6                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               | Db 601                          | EESEATPSPVLPDIVMEAPLNSAVPSAGASVIQPSSSPLEASSVNYESIKHEPENPPPYE 660     |
| ; Patent No. USPATIONAL OF STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STA | Oy 172                          | 171                                                                  |
| , CINCLOL INFORMATION.  A APPLICAT: STRITIVATION: NOCO-BECEPHON M.  TITIE OF INVENTION: NOCO-BECEPHOD MENTARED BLOCKADE OF AVOINT CERTER.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      | Db 661                          | EAMSVSLKKVSGIKEEIKEPENINAALQETEAPYISIACDLIKETKLSAEPAPDFSDYSE 720     |
| ; FILE REFERENCE: COT7 CIP US. ; FILE REFERENCE: COT7 CIP US. ; CIPDENT ADDITIONATION NUMBER: 115/00/072 COM                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   | Oy 172                          | 171                                                                  |
| ; CURRENT FILLION NOTION: 0.5/03/274; CURRENT FILLION DATE: 2.001-107/03/274; DIDIOR ADDITONATON NUMBER: DAM/HEGA/A1044                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        | Db 721                          | MAKVEQPVPDHSELVEDSSPDSEPVDLFSDDSIPDVPQKQDETVMLVKESLTETSFESMI 780     |
| ; PRIOR FILING DATE: DOUGHER: FULLOSOL/ULO41 ; PRIOR FILING DATE: DOUGH-01-12 . BDIOR ABDITTANTON WIMMEDD: AAA                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 | Oy 172                          | 171                                                                  |
| FALCA PILICALION NOMBER: 09/190,140 PRIOR FILING BATE: 2001-01-12 PRIOR ADDITORATON WIMMED: 6/202 370                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          | Db 781                          | EYENKEKLSALPPEGGKPYLESFKLSLDNTKDTLLPDEVSTLSKKEKIPLQMEELSTAVY 840     |
| ; FRICK AFFLICATION NUMBER: 00/230,3/8 ; PRIOR FILING DATE: 2000-09-29 ; DRIOR DATE: 2000-09-29                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                | Oy 172                          | 171                                                                  |
| FRICK AFFLICATION NUMBER: 00/20/,300 ; PRIOR FILING DATE: 2000-05-26 ; FRICK FILING DATE: 2000-05-26                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           | Db 841                          | SNDDLFISKEAQIRETETFSDSSPIELIDEFPTLISSKTDSFSKLAREYTDLEVSHKSEI 900     |
| ; PRIOR AFFLICATION NUMBER: 60,175,707<br>; PRIOR FILING DATE: 2000-01-12                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      | Oy 172                          | 171                                                                  |
| ; NOTHER OF SEQ ID NOS: 5/<br>SOFTWARE: Patentin Ver. 2.1                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      | Db 901                          | ANAPDGAGSLPCTELPHDLSLKNIQPKVEEKISFSDDFSKNGSATSKVLLLPPDVSALAT 960     |
| ; LENGTH: 1192<br>; TENGTH: 1192<br>; TYDE: DPT                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                | . Qy 172                        | TSVVDLLYWRDIKKTGVV 189                                               |
| ; ORGANISM: Homo sapiens<br>US-09-972-599A-6                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   | Db 961                          | QAEIESIVKPKVLVKEAEKKLPSDTEKEDRSPSAIFSAELSKTSVVDLLYWRDIKKTGVV 1020    |
| 95.0%; Score 1756.9; DB 9; Length 1192;                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        |                                 | PGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQAIQKSDEGHPFRAYLESE 249<br> |
| VACIVE O, MIDHACCHES O, INCELS VSSSDSPRRPQPAFKYQFVREPEDEEEEEEEEEEDEDEDEDI                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      | PA 60 Dh 1081                   | VAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDSLKFAVLMMVFTYVGALFNGLTL 309     |
| Db 1 MEDLDQSPLVSSSDSPRPQPAFKYQFVREPEDEEEEEEEEEEEEEDEDEDLEELEVLERKF                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             | 09                              |                                                                      |
| Qy 61 AGLSAAPVPTAPAAGAPLADFGNDFVPPARGPLPAAPPVAPERQPSWDFSPVSSTVPAP                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              | 120 QY 310<br>120 Db 1141       | LILALISLESVPVIYERHQAQIDHYLGLANKAVKDAAKIQAKIPGLKRKAE 361<br>          |
| Qy 121 SPLSAAAVSPSKLPEDDEPPARPPPPPASVSPQAEPVWTPPAPAPPS                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         | RESULT 13                       | 1.                                                                   |
|                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                | 180                             | /i<br>Application US/10060036<br>No. US20030073144A1                 |
| Qy 172                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         | 171 ; GENERAL INFO ; APPLICANT: | NRMATION:<br>Benson, Darin R.                                        |
|                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                | 240 ; APPLICANT ; APPLICANT     | : Kalos, Michael D. : Lodes, Michael J.                              |
| 0y 172                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         | 171 ; APPLICANT:                | Persing, David H.<br>Hepler, William T.                              |

| QY         172                                                                                                                                                                                                                                                                                                                                                                | Qy         190 FGASLFLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQAIQKSDEGHPFRAYLESE 249           Db         1021 FGASLFLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQAIQKSDEGHPFRAYLESE 1080           Qy         250 VAISBELVQKYSNSALGHVNCTIKELRRLFLVDDLVDSLKFAVLMWVFTYVGALFNGLTL 309           Db         1081 VAISBELVQKYSNSALGHVNCTIKELRRLFLVDDLVDSLKFAVLMWVFTYVGALFNGLTL 1140           Qy         310 LILALISLESVPVIYERHQAQIDHYLGLANKAVKDAMAKIQAKIPGLKRKAE 361           Db         1141 LILALISLESVPVIYERHQAQIDHYLGLANKAVKDAMAKIQAKIPGLKRKAE 1192 | RESULT 14 US-10-267-502-429  is Sequence 429, Application US/10267502  is Publication No. US20040071700A1  is GENERAL INFORMATION:  is APPLICANT: Kim, Jaesecob  it TILE OF INVENTION: Obesity Linked Genes  if TILE OF INVENTION: Obesity Linked Genes  if TILE OF INVENTION: Obesity Linked Genes  if CURRENT APPLICATION NUMBER: US/10/267,502  if CURRENT FILING DATE: 2003-01-27  if NUMBER OF SEQ ID NOS: 439  if SOFWRARE: Patentin version 3.2 | 429 1192 1 Homo sapiens 2-429 Similarity 30.3% 61; Conservative 1 MEDLDQSPLVSSSDSPP! | Qy         61 AGLSAAPVPTAPAGAPLMDFGNDFVPPABRGPLPAAPPVAPERQBSWDPSFVSSTVPAP 120           Db         61 AGLSAAPVPTAPAAGAPLMDFGNDFVPPABRGPLPAAPPVAPERQPSWDPSFVSSTVPAP 120           Qy         121 SPLSAAAVSPSKLPEDDBPPARPPPPPASVSPQAEPWTPPAPAPAPS         171           Db         121 SPLSAAAVSFSKLPEDDEPPARPPPPPASVSPQAEPWTPPAPAPAPARPS         171           OV         172 | 181 SSGSVDETLFALPAASEPVIRSSAENMDLKEQPGNTISAGGEDFPSVLLETAASLPSLSP 172 |
|-------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|---------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|--------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|--------------------------------------------------------------------------------------|------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|----------------------------------------------------------------------|
| ; APPLICANT: Jiang, Yuqiu ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY ; TITLE OF INVENTION: AND DIAGNOSIS OF PANCREATIC CANCER ; FILE REFERENCE: 210121.566 ; CURRENT APPLICATION NUMBER: US/10/060,036 ; CURRENT FILING DATE: 2002-01-30 ; NUMBER OF SEQ ID NOS: 4560 ; SEQ ID NO 71 ; LENGTH: 1192 ; TYPE: PRT ; ORGANISM: Homo sapiens US-10-060-036-71 | Query Match         95.0%;         Score 1756.9;         DB 14;         Length 1192;           Best Local Similarity         30.3%;         Pred. No. 3.2e-52;         Indels 831;         Gaps         1;           QY         1 MEDLDQSPLVSSDSPRRQPAFKYQFVREPEDEREREREBEBEBELELELERKERAR 60                                                                                                                                                                                                                                         | Qy         121 SPLSAAAVSPSKLPEDDEPPRASVSPQAEPVWTPPAAPAPAPAS         171           Db         121 SPLSAAAVSPSKLPEDDEPPARPPPPPASVSPQAEPVWTPPABAPAPAPRRRG 180           Qy         172                                                                                                                                                                                                                                                                    | 301 GSSFSVSPKAESAVIVANPREEIIVKNKDEEEKLVSNNILHNQQELPTALTKLVKEDEVV 172                 | DB 481 PLIGDPISENKIDEKKIEEKKAQIVIEKNISIKISNPFLVAAQDSEIDYVTIDNLTKVIE 540  QY 172                                                                                                                                                                                                                                                                                              | QY         172                                                       |

| Db         361 SSEKA           Qy         172           Db         421 DKKCF           Qy         172           Db         541 EVVANI           Qy         172           Db         601 EESEA           Qy         172           Db         601 EESEA           Qy         172           Db         661 EAMSW           Qy         172           Db         721 MAKVE           Qy         172           Db         721 MAKVE           Qy         172           Db         781 EYENKO           Qy         172           Db         781 EYENKO           Qy         172           Db         781 EYENKO           Qy         172           Db         781 EYENKO |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                | ; TYPE: PRT ; TANDESTONISM: Homo Bapie US-10-327-213-9 Query Match Best Local Similarity Matches 361; Conserv | sapiens<br>95<br>arity 30       |
|-------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|--------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|---------------------------------------------------------------------------------------------------------------|---------------------------------|
| 172 421 DK 421 DK 172 172 172 172 172 172 172 172 172 172 172 172 172                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                | -10-32/-213-9<br>Query Match<br>Best Local Simi<br>Matches 361;                                               | 95.<br>arity 30.<br>onservative |
| 421 DX 172 172 172 172 172 172 172 172 172 172 172 172 172 172                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                | nccn<br>al Simi<br>361;                                                                                       | 4                               |
| 172 481 PL 172 172 172 172 172 172 172 172 172 172 172 172 172                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                | 361;                                                                                                          |                                 |
| 481 PL 172 172 172 172 172 172 172 172 172 172 172 172                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                | •                                                                                                             | · + > > + DOITO                 |
| 172 541 BV 172 172 172 172 172 172 172 173 173                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |                                                                                                               | 1 MEDLDQSPLVSSSDS               |
| 541 BV<br>172<br>172<br>172<br>172<br>172<br>172<br>172<br>172                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                | <b>-</b> 1 ;                                                                                                  | DOSPLVSSSD                      |
| 172 601 EB 172 172 172 172 172 172 172 172                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                | 61                                                                                                            | AGLSAAPVPTAPAAG                 |
| 601 EB<br>172<br>661 EA<br>172<br>721 MA<br>172<br>172                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                | 19                                                                                                            | AGLSAAPVPTAPAAG                 |
| 172<br>661 BA<br>172<br>721 MA<br>172<br>781 BY                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   | SEATFSFVLPDIVMEAPLNSAVPSAGASVIQPSSSPLEASSVNYESIKHEPENPPPYE 660                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 | 121                                                                                                           | SPLSAAVSPSKLPE                  |
| 661 BA<br>172<br>721 MA<br>172<br>781 BY                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          | 171                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            | 121                                                                                                           | AAAVSPSKLPI                     |
| 172<br>721 MA<br>172<br>781 BY                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    | MSVSLKKVSGIKEEIKEPENINAALQETEAPYISIACDLIKETKLSAEPAPDFSDYSE 720                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 | 172                                                                                                           |                                 |
| 721 MA<br>172<br>181 EY<br>172                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    | 171                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            | 181                                                                                                           | SSGSVDETLFALPAA                 |
| 172<br>781 EY<br>172                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              | KVEQPVPDHSELVEDSSPDSEPVDLFSDDSIPDVPQKQDETVMLVKESLTETSFESMI 780                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 | 172                                                                                                           |                                 |
| 781 EY                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            | 171                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            | 241                                                                                                           | LSAASFKEHEYLGNL                 |
|                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   | ENKEKLSALPPEGGKPYLESFKLSLDNTKDTLLPDEVSTLSKKEKIPLQMEELSTAVY 840                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 | Qy 172                                                                                                        |                                 |
|                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   | 171                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            | 301                                                                                                           | GSSFSVSPKAESAVI                 |
| 841 SN                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            | DDLF1SKEAQIRETETFSDSSPIEIIDEPPTL1SSKTDSFSKLAREYTDLEVSHKSEI 900                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 | Qy 172                                                                                                        |                                 |
| 172                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                | Db 361 SSEKA                                                                                                  | SSEKAKDSFNEKRVA                 |
| NA 106                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            | APDGAGSLPCTELPHDLSLKNIOPKVEEKISFSDDFSKNGSATSKVLLLPPDVSALAT 960                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 | Oy 172                                                                                                        |                                 |
| ;                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                | Db 421 DKKCF                                                                                                  | DKKCFADSLEQTNHE                 |
| 1,2<br>961 OA                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                | Qy 172                                                                                                        |                                 |
| 061                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                | Db 481 PLLGD                                                                                                  | PLLGDPTSENKTDEK                 |
| 1001                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                | Qy 172                                                                                                        |                                 |
| 47 05C                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                | Db 541 EVVAN                                                                                                  | EVVANMPEGLTPDLV                 |
| 252<br>                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           | TOTAL VOICE STATE OF THE TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL | Qy 172                                                                                                        |                                 |
| 11010                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                | Db 601 EESEA                                                                                                  | EESEATPSPVLPDIV                 |
| 1 1 1                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             | THE TOTAL OF ALL LEGIT LINES AND ALL LEGIT LANGES AND ALL LEGIT LANGES AND ALL LEGIT LANGES AND ALL LEGIT LANGES AND ALL LEGIT LANGES AND ALL LEGIT LANGES AND ALL LEGIT LANGES AND ALL LEGIT LANGES AND ALL LEGIT LANGES AND ALL LEGIT LANGES AND ALL LEGIT LANGES AND ALL LEGIT LANGES AND ALL LEGIT LANGES AND ALL LEGIT LANGES AND ALL LEGIT LANGES AND ALL LEGIT LANGES AND ALL LEGIT LANGES AND ALL LEGIT LANGES AND ALL LEGIT LANGES AND ALL LEGIT LANGES AND ALL LEGIT LANGES AND ALL LEGIT LANGES AND ALL LEGIT LANGES AND ALL LEGIT LANGES AND ALL LEGIT LANGES AND ALL LEGIT LANGES AND ALL LEGIT LANGES AND ALL LEGIT LANGES AND ALL LEGIT LANGES AND ALL LEGIT LANGES AND ALL LEGIT LANGES AND ALL LEGIT LANGES AND ALL LEGIT LANGES AND ALL LEGIT LANGES AND ALL LEGIT LANGES AND ALL LEGIT LANGES AND ALL LEGIT LANGES AND ALL LEGIT LANGES AND ALL LEGIT LANGES AND ALL LEGIT LANGES AND ALL LEGIT LANGES AND ALL LEGIT LANGES AND ALL LEGIT LANGES AND ALL LEGIT LANGES AND ALL LEGIT LANGES AND ALL LEGIT LANGES AND ALL LEGIT LANGES AND ALL LEGIT LANGES AND ALL LEGIT LANGES AND ALL LEGIT LANGES AND ALL LEGIT LANGES AND ALL LEGIT LANGES AND ALL LEGIT LANGES AND ALL LEGIT LANGES AND ALL LEGIT LANGES AND ALL LEGIT LANGES AND ALL LEGIT LANGES AND ALL LEGIT LANGES AND ALL LEGIT LANGES AND ALL LEGIT LANGES AND ALL LEGIT LANGES AND ALL LEGIT LANGES AND ALL LEGIT LANGES AND ALL LEGIT LANGES AND ALL LEGIT LANGES AND ALL LEGIT LANGES AND ALL LEGIT LANGES AND ALL LEGIT LANGES AND ALL LEGIT LANGES AND ALL LEGIT LANGES AND ALL LEGIT LANGES AND ALL LEGIT LANGES AND ALL LEGIT LANGES AND ALL LEGIT LANGES AND ALL LEGIT LANGES AND ALL LEGIT LANGES AND ALL LEGIT LANGES AND ALL LEGIT LANGES AND ALL LEGIT LANGES AND ALL LEGIT LANGES AND ALL LEGIT LANGES AND ALL LEGIT LANGES AND ALL LEGIT LANGES AND ALL LEGIT LANGES AND ALL LEGIT LANGES AND ALL LEGIT LANGES AND ALL LEGIT LANGES AND ALL LEGIT LANGES AND ALL LEGIT LANGES AND ALL LEGIT LANGES AND ALL LEGIT LANGES AND ALL LEGIT LANGES AND ALL LEGIT LANGES AND ALL LEGIT LANGES AND ALL LEGIT LANGES AND ALL LEGIT LANGES A | Qy 172                                                                                                        |                                 |
|                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   | TODE OVE VII BENINGAÇIDII DOMENNAV KOMPINAKA ÇANALE GIRKAKAS                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   | Db 661 EAMSV                                                                                                  | EAMSVSLKKVSGIKE                 |
| RESULT 15                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                | Qy 172                                                                                                        |                                 |
| Sequence 9, Application US/10327213                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               | cation US/10327213                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             | Db 721 MAKVE(                                                                                                 | MAKVEQPVPDHSELVI                |
| GENERAL INFORMATIC                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                | ATION:                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         | Oy 172                                                                                                        |                                 |
|                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   | NICONI, MARCO                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  | Db 781 EYENKO                                                                                                 | EYENKEKLSALPPEG                 |
|                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   | TITLE OF INVENTION: INHIBITORS OF MYELIN-ASSOCIATED GLYCOPROTEIN (MAG) TITLE OF INVENTION: ACTIVITY FOR PRITIATING NEIBBL GROWTH AND BEGENERATION                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              | Qy 172                                                                                                        |                                 |
|                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   | CUNY/003                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       | Db 841 SNDDE                                                                                                  | SNDDLFISKEAQIRE                 |
| CURRENT FILING D                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  | CURRENT FILING DATE: 2002-12-20                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                | Oy 172                                                                                                        |                                 |
| SOFTWARE: Patent:                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 | nos: 45<br>In Ver. 2.1                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         | Db 901 ANAPDO                                                                                                 | ANAPDGAGSLPCTEL                 |

```
GAPLMDFGNDFVPPAPRGPLPAAPPVAPERQPSWDFSPVSSTVPAP 120
 EDDEPPARPPPPPASVSPQAEPVWTPPAPAAPPS----- 171
 EKDSESSNDDTSFPSTPEGIKDRPGAYITCAPFNPAATESIATNIF 480
 VQEACESELNEVTGTKIAYETKMDLVQTSEVMQESLYPAAQLCPSF 600
 ASEPVIRSSAENMDLKEQPGNTISAGQEDFPSVLLETAASLPSLSP 240
 171
 LSTVLPTEGTLOENVSEASKEVSEKAKTLLIDRDLTEFSELEYSEM 300
 IVANPREEIIVKNKDEEEKLVSNNILHNQQELPTALTKLVKEDEVV 360
 AVEAPMREEYADFKPFERVWEVKDSKEDSDMLAAGGKIESNLESKV 420
 KKIEEKKAQIVTEKNTSTKTSNPFLVAAQDSETDYVTTDNLTKVTE 540
 171
 VMEAPLNSAVPSAGASVIQPSSSPLEASSVNYESIKHEPENPPPYE 660
 EEIKEPENINAALOETEAPYISIACDLIKETKLSABPAPDFSDYSE 720
 171
 171
 VEDSSPDSEPVDLFSDDSIPDVPQKQDETVMLVKESLTETSFESMI 780
 171
 GGKPYLESFKLSLDNTKDTLLPDEVSTLSKKEKIPLQMEELSTAVY 840
 ETETFSDSSPIEIIDEFPTLISSKTDSFSKLAREYTDLEVSHKSEI 900
 LPHDLSLKNIQPKVEEKISFSDDFSKNGSATSKVLLLPPDVSALAT 960
 SPPROQPAFKYQFVREPEDEBEBEBEBEBEBDBDBDLBBLBVLERKPA 60
 SPPRPQPAFKYQFVREPEDEEEEEEEBBDBDLEELBVLERKPA 60
.0%; Score 1756.9; DB 16; Length 1192;
0.3%; Pred. No. 3.2e-52;
e 0; Mismatches 0; Indels 831; Gaps
```

| TSTATE TO THE TOTAL TRANSPORT TO THE THE THE THE THE THE THE THE THE THE | 961 QAEIESIVKPKVLVKEAEKKLPSDTEKEDRSPSAIFSAELSKTSVVDLLYWRDIKKTGVV 1020 | 190 FGASLPLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQALQKSDEGHPFRAYLESE 249 | 1021 FGASLFLLISLTVFSIVSYTAYIALALLSVTISFRIYKGVIQAIQKSDEGHPFRAYLESE 1080 | 250 VAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDSLKFAVLMMVFTVVGALFNGLTL 309 | 1081 VAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDSLKFAVLMWVFTYVGALFNGLTL 1140 | 310 LILALISLESVPVIYERHQAQIDHYLGLANKOVKDAMAKIQAKIPGLKRKAE 361 | 1141 LILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAKIPGLKRKAE 1192 |  |
|--------------------------------------------------------------------------|-----------------------------------------------------------------------|----------------------------------------------------------------------|------------------------------------------------------------------------|----------------------------------------------------------------------|------------------------------------------------------------------------|--------------------------------------------------------------|----------------------------------------------------------------|--|
| 172                                                                      | 961                                                                   | 190                                                                  | 1021                                                                   | 250                                                                  | 1081                                                                   | 310                                                          | 1141                                                           |  |
| ò                                                                        | g                                                                     | à                                                                    | q <sub>Q</sub>                                                         | Š                                                                    | qq                                                                     | ò                                                            | qa                                                             |  |

Search completed: June 23, 2005, 10:34:33 Job time: 114.151 secs

```
June 23, 2005, 10:16:50; Search time 114.158 Seconds (without alignments) 1223.045 Million cell updates/sec
 1850
1 MEDLDQSPLVSSSDSPPRPQ.....VKDAMAKIQAKIPGLKRKAE 361
GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
 Total number of hits satisfying chosen parameters:
 2105692 segs, 386760381 residues
 protein search, using sw model
 Gapop 10.0 , Gapext 0.1
 US-09-830-972-29-FUSED
 seq length: 0
seq length: 200000000
 BLOSUM62
 Perfect score:
Sequence:
 Scoring table:
 1
 Minimum DB Maximum DB M
 OM protein
 Searched:
 Run on:
```

A\_Geneseq\_16Dec04:\* geneseqp2003as:\* geneseqp2003bs:\* geneseqp2004s:\* geneseqp1980s:\* geneseqp1990s:\* geneseqp2000s:\* geneseqp2001s:\* geneseqp2002s:\* ...... Database

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

|           | Description         | Aay53624 A bone ma | Aay56969 Human MAG | Aab24242 Human Nog |          | Aam47954 Human RTN | Abp68601 Human pan | Human    | Human    | 3 Human  | Adp67235 Human Nog | 7 Human  | Human    | Aab82349 Human NOG | Human    | Human    | Human    | Human    | . Abr59667 Human Nog | Ado08103 Human pol | 1 Human  | 4 Human  | 6 Human  | Adk67502 Human RTN | Ado26400 Human tru | Aay71311 Human neu |
|-----------|---------------------|--------------------|--------------------|--------------------|----------|--------------------|--------------------|----------|----------|----------|--------------------|----------|----------|--------------------|----------|----------|----------|----------|----------------------|--------------------|----------|----------|----------|--------------------|--------------------|--------------------|
| SUMMARIES | ID                  | AAY53624           | AAY56969           | AAB24242           | AAB82350 | AAM47954           | ABP68601           | ABB81079 | ADI63044 | ADK67503 | ADP67235           | ABG30937 | AAY56967 | AAB82349           | AAU04591 | ABG30938 | ABP68600 | ABB81078 | ABR59667             | AD008103           | ADP45551 | ADP67234 | ADR13966 | ADK67502           | AD026400           | AAY71311           |
|           | DB                  | m                  | ٣                  | ო                  | 4        | Ŋ                  | Ŋ                  | Ŋ        | 7        | 7        | œ                  | ß        | ٣        | 4                  | 4        | ß        | ഹ        | w        | 9                    | œ                  | æ        | œ        | æ        | 7                  | œ                  | Э                  |
|           | Length              | 373                | 373                | 373                | 373      | 373                | 373                | 373      | 373      | 373      | 373                | 373      | 1192     | 1192               | 1192     | 1192     | 1192     | 1192     | 1192                 | 1192               | 1192     | 1192     | 1192     | 1192               | 1192               | 1178               |
|           | %<br>Query<br>Match | 99.1               | 99.1               | 99.1               | 99.1     | 99.1               | 99.1               | 99.1     | 99.1     | 99.1     | 99.1               | 98.7     | 95.0     | 95.0               | 95.0     | 95.0     | S.       | 95.0     | 95.0                 | 95.0               | 95.0     | 95.0     | 95.0     | 94.6               | 94.6               | 94.6               |
|           | Score               | 1833.8             | 1833.8             | 1833.8             | 1833.8   | 1833.8             | 1833.8             | 1833.8   | 1833.8   | 1833.8   | 1833.8             | 1825.8   | 1756.9   | 1756.9             | 1756.9   | 1756.9   | 1756.9   | 1756.9   | 1756.9               | 1756.9             | 1756.9   | 1756.9   | 1756.9   | 1749.9             | 1749.9             | 1749.3             |
|           | Result<br>No.       |                    | 7                  | ٣                  | 4        | S                  | 9                  | 7        | 8        | σv       | 10                 | 11       | 12       | 13                 | 14       | 15       | 16       |          | 18                   | 19                 | 20       |          | 22       |                    | 24                 | 25                 |

AAY53622-43 represent bone marrow secreted proteins of human bone marrow stromal cells. The proteins can exhibit cytokine, cell proliferation, or cell differentiation activity (either inducing or inhibiting). They can

Claim 2; Page 74; 120pp; English.

| Adb85283 Rat fooce Aay71385 Alternati Aay71358 Rat Nogo Aay71383 Rat neuro Aab81076 Rat neuro Aa90397 Human gen Aay71310 Rat neuro Aay71310 Rat neuro Ado20397 Rat neuro Ado20399 Rat trunc Ado45572 Rat Nogo Ady11557 Rat Nogo Ady11557 Rat Nogo Ady11557 Rat Nogo Ady11557 Rat Nogo Ady11557 Rat Nogo Ady11557 Rat Nogo Ady11557 Rat Nogo Ady11557 Rat Nogo Ady11557 Rat Nogo Ady11557 Rat Nogo Ady11557 Rat Nogo Ady11557 Rat Nogo Ady11557 Rat Nogo Ady11557 Rat Nogo Ady11557 Rat Nogo Ady11557 Rat Nogo Ady11557 Rat Nogo Ady11557 Rat Nogo Ady11557 Rat Nogo Ady11557 Rat Nogo Ady11557 Rat Nogo Ady16450 Fuelon pro Ady16420 Fuelon pro Ady16420 Fuelon pro Ady16420 Fuelon pro Ady16420 Fuelon pro Ady16420 Fuelon pro Ady16420 Fuelon pro Ady16420 Fuelon pro Ady16420 Fuelon pro Ady16420 Fuelon pro Ady16420 Fuelon pro Ady16420 Fuelon pro Ady16420 Fuelon pro Ady16420 Fuelon pro Ady16420 Fuelon pro Ady16420 Fuelon pro Ady16420 Fuelon pro Ady16420 Fuelon pro Ady16420 Fuelon pro Ady16420 Fuelon pro Ady16420 Fuelon pro Ady16420 Fuelon pro Ady16420 Fuelon pro Ady16420 Fuelon pro Ady16420 Fuelon pro Ady16420 Fuelon pro Ady16420 Fuelon pro Ady16420 Fuelon pro Ady16420 Fuelon pro Ady16420 Fuelon pro Ady16420 Fuelon pro Ady16420 Fuelon pro Ady16420 Fuelon pro Ady16420 Fuelon pro Ady16420 Fuelon pro Ady16420 Fuelon pro Ady16420 Fuelon pro Ady16420 Fuelon pro Ady16420 Fuelon pro Ady16420 Fuelon pro Ady16420 Fuelon pro Ady16420 Fuelon pro Ady16420 Fuelon pro Ady16420 Fuelon pro Ady16420 Fuelon pro Ady16420 Fuelon pro Ady16420 Fuelon pro Ady16420 Fuelon pro Ady16420 Fuelon pro Ady16420 Fuelon pro Ady16420 Fuelon pro Ady16420 Fuelon pro Ady16420 Fuelon pro Ady16420 Fuelon pro Ady16420 Fuelon pro Ady16420 Fuelon pro Ady16420 Fuelon pro Ady16420 Fuelon pro Ady16420 Fuelon pro Ady16420 Fuelon pro Ady16420 Fuelon pro Ady16420 Fuelon pro Ady16420 Fuelon pro Ady16420 Fuelon pro Ady16420 Fuelon pro Ady16420 Fuelon pro Ady16420 Fuelon pro Ady16420 Fuelon pro Ady16420 Fuelon pro Ady16420 Fuelon pro Ady16420 Fuelon pro Ady16420 Fuelon pro Ady16420 Fuelon pro Ad                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             | •        |
|--------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|----------|
| ADB85283<br>AAY71385<br>AAY71385<br>AAY71383<br>ABB1076<br>AABB1076<br>AAY71310<br>AAY71310<br>AAY71310<br>AAY71384<br>ADC26399<br>ADP45572<br>AAY71557<br>AAY71557<br>AAY71557<br>AAY71557<br>AAY71557<br>AAY11557<br>AAY11557<br>AAY11557<br>AAY11557<br>ADO8105<br>AAY80537<br>AAY80537<br>AAY80537<br>AAY80537                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         | PEOLICIA |
|                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            | 2        |
| 33,000<br>33,000<br>33,000<br>33,000<br>33,000<br>33,000<br>33,000<br>33,000<br>33,000<br>33,000<br>33,000<br>33,000<br>33,000<br>33,000<br>33,000<br>33,000<br>33,000<br>33,000<br>34,000<br>34,000<br>34,000<br>34,000<br>34,000<br>34,000<br>34,000<br>34,000<br>34,000<br>34,000<br>34,000<br>34,000<br>34,000<br>34,000<br>34,000<br>34,000<br>34,000<br>34,000<br>34,000<br>34,000<br>34,000<br>34,000<br>34,000<br>34,000<br>34,000<br>34,000<br>34,000<br>34,000<br>34,000<br>34,000<br>34,000<br>34,000<br>34,000<br>34,000<br>34,000<br>34,000<br>34,000<br>34,000<br>34,000<br>34,000<br>34,000<br>34,000<br>34,000<br>34,000<br>34,000<br>34,000<br>34,000<br>34,000<br>34,000<br>34,000<br>34,000<br>34,000<br>34,000<br>34,000<br>34,000<br>34,000<br>34,000<br>34,000<br>34,000<br>34,000<br>34,000<br>34,000<br>34,000<br>34,000<br>34,000<br>34,000<br>34,000<br>34,000<br>34,000<br>34,000<br>34,000<br>34,000<br>34,000<br>34,000<br>34,000<br>34,000<br>34,000<br>34,000<br>34,000<br>34,000<br>34,000<br>34,000<br>34,000<br>34,000<br>34,000<br>34,000<br>34,000<br>34,000<br>34,000<br>34,000<br>34,000<br>34,000<br>34,000<br>34,000<br>34,000<br>34,000<br>34,000<br>34,000<br>34,000<br>34,000<br>34,000<br>34,000<br>34,000<br>34,000<br>34,000<br>34,000<br>34,000<br>34,000<br>34,000<br>34,000<br>34,000<br>34,000<br>34,000<br>34,000<br>34,000<br>34,000<br>34,000<br>34,000<br>34,000<br>34,000<br>34,000<br>34,000<br>34,000<br>34,000<br>34,000<br>34,000<br>34,000<br>34,000<br>34,000<br>34,000<br>34,000<br>34,000<br>34,000<br>34,000<br>34,000<br>34,000<br>34,000<br>34,000<br>34,000<br>34,000<br>34,000<br>34,000<br>34,000<br>34,000<br>34,000<br>34,000<br>34,000<br>34,000<br>34,000<br>34,000<br>34,000<br>34,000<br>34,000<br>34,000<br>34,000<br>34,000<br>34,000<br>34,000<br>34,000<br>34,000<br>34,000<br>34,000<br>34,000<br>34,000<br>34,000<br>34,000<br>34,000<br>34,000<br>34,000<br>34,000<br>34,000<br>34,000<br>34,000<br>34,000<br>34,000<br>34,000<br>34,000<br>34,000<br>34,000<br>34,000<br>34,000<br>34,000<br>34,000<br>34,000<br>34,000<br>34,000<br>34,000<br>34,000<br>34,000<br>34,000<br>34,000<br>34,000<br>34,000<br>34,000<br>34,000<br>34,000<br>34,000<br>34,000<br>34,000<br>34,000<br>34,000<br>34,000<br>34,000<br>34,000<br>34,000<br>34,000<br>34,000<br>34,000<br>34,000<br>34,000<br>34,000<br>34,000<br>34,000<br>34,000<br>34,000<br>34,000<br>34,000<br>34,000<br>34,000<br>34,000<br>34,000<br>34,000<br>34,000<br>34,000<br>34,000<br>34,000<br>34,000<br>34,000<br>34,000<br>34,000<br>34,000<br>34,000<br>34,000<br>34,000<br>34,000<br>34,000<br>34,000<br>34,000<br>34,000<br>34,000<br>34,000<br>34,000<br>34,000<br>34,000<br>34,000<br>34,000<br>34,000<br>34,000<br>34,000<br>34,000<br>34,000<br>34,000<br>34,000<br>34,000<br>34,000<br>34,000<br>34,000<br>34,000<br>34,000<br>34,000<br>34,000<br>34,000<br>34,000<br>34,000<br>34,000<br>34,000<br>34,000<br>34,000<br>34,000<br>34,000<br>34,000<br>34,000<br>34,000<br>34,000<br>34 | 3        |
| 8888833.1<br>88833.2<br>90.0<br>90.0<br>90.0<br>90.0<br>90.0<br>90.0<br>90.0<br>90                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         | 2        |
|                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            |          |
| 11556.2<br>11551.6<br>11551.6<br>11551.6<br>11551.6<br>11556.3<br>11556.3<br>11556.3<br>11556.3<br>11556.3<br>11556.3<br>11556.3<br>11556.3<br>11556.3<br>11556.3<br>11556.3<br>11556.3<br>11556.3<br>11556.3<br>11556.3<br>11556.3<br>11556.3<br>11556.3<br>11556.3<br>11556.3<br>11556.3<br>11556.3<br>11556.3<br>11556.3<br>11556.3<br>11556.3<br>11556.3<br>11556.3<br>11556.3<br>11556.3<br>11556.3<br>11556.3<br>11556.3<br>11556.3<br>11556.3<br>11556.3<br>11556.3<br>11556.3<br>11556.3<br>11556.3<br>11556.3<br>11556.3<br>11556.3<br>11556.3<br>11556.3<br>11556.3<br>11556.3<br>11556.3<br>11556.3<br>11556.3<br>11556.3<br>11556.3<br>11556.3<br>11556.3<br>11556.3<br>11556.3<br>11556.3<br>11556.3<br>11556.3<br>11556.3<br>11556.3<br>11556.3<br>11556.3<br>11556.3<br>11556.3<br>11556.3<br>11556.3<br>11556.3<br>11556.3<br>11556.3<br>11556.3<br>11556.3<br>11556.3<br>11556.3<br>11556.3<br>11556.3<br>11556.3<br>11556.3<br>11556.3<br>11556.3<br>11556.3<br>11556.3<br>11556.3<br>11556.3<br>11556.3<br>11556.3<br>11556.3<br>11556.3<br>11556.3<br>11556.3<br>11556.3<br>11556.3<br>11556.3<br>11556.3<br>11556.3<br>11556.3<br>11556.3<br>11556.3<br>11556.3<br>11556.3<br>11556.3<br>11556.3<br>11556.3<br>11556.3<br>11556.3<br>11556.3<br>11556.3<br>11556.3<br>11556.3<br>11556.3<br>11556.3<br>11556.3<br>11556.3<br>11556.3<br>11556.3<br>11556.3<br>11556.3<br>11556.3<br>11556.3<br>11556.3<br>11556.3<br>11556.3<br>11556.3<br>11556.3<br>11556.3<br>11556.3<br>11556.3<br>11556.3<br>11556.3<br>11556.3<br>11556.3<br>11556.3<br>11556.3<br>11556.3<br>11556.3<br>11556.3<br>11556.3<br>11556.3<br>11556.3<br>11556.3<br>11556.3<br>11556.3<br>11556.3<br>11556.3<br>11556.3<br>11556.3<br>11556.3<br>11556.3<br>11556.3<br>11556.3<br>11556.3<br>11556.3<br>11556.3<br>11556.3<br>11556.3<br>11556.3<br>11556.3<br>11556.3<br>11556.3<br>11556.3<br>11556.3<br>11556.3<br>11556.3<br>11556.3<br>11556.3<br>11556.3<br>11556.3<br>11556.3<br>11556.3<br>11556.3<br>11556.3<br>11556.3<br>11556.3<br>11556.3<br>11556.3<br>11556.3<br>11556.3<br>11556.3<br>11556.3<br>11556.3<br>11556.3<br>11556.3<br>11556.3<br>11556.3<br>11556.3<br>11556.3<br>11556.3<br>11556.3<br>11556.3<br>11556.3<br>11556.3<br>11556.3<br>11556.3<br>11556.3<br>11556.3<br>11556.3<br>11556.3<br>11556.3<br>11556.3<br>11556.3<br>11556.3<br>11556.3<br>11556.3<br>11556.3<br>11556.3<br>11556.3<br>11556.3<br>11556.3<br>11556.3<br>11556.3<br>11556.3<br>11556.3<br>11556.3<br>11556.3<br>11556.3<br>11556.3<br>11556.3<br>11556.3<br>11556.3<br>11556.3<br>11556.3<br>11556.3<br>11556.3<br>11556.3<br>11556.3<br>11556.3<br>11556.3<br>11556.3<br>11556.3<br>11556.3<br>11556.3<br>11556.3<br>11556.3<br>11556.3<br>11556.3<br>11556.3<br>11556.3<br>11556.3<br>11556.3<br>11556.3<br>11556.3<br>11556.3<br>11556.3<br>11556.3<br>11556.3<br>11556.3<br>11556.3<br>11556.3<br>11556.3<br>11556.3<br>11556.                                                                                                                | 401      |
| 00000000000000000000000000000000000000                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     | 7        |
|                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            |          |

## ALIGNMENTS

Bone marrow secreted protein; bone marrow stromal cell; cytokine; cell proliferation; cell differentiation; hematopoiesis; anaemia; myeloid cell deficiency; lymphoid cell deficiency; myeloid cell; erythroid progenitor cell; colony stimulating factor; granulocyte; monocyte; macrophage; myelo-euppression; megakaryocyte; platelet; platelet disorder; thrombocytopenia; hematopoeitic stem cell; stem cell disorder; aplastic anaemia; bone differentiation; parcoxysmal nocturnal hemoglobinuria; bone growth; cartilage; tendon; ligament; nerve; wound healing; tissue repair; burn; incision; ulcer; bone fracture; cartilage damage; artificial joint. New isolated human polynucleotide and secreted proteins can induce production of other cytokines in certain cell populations. bone marrow secreted protein designated BMS112 AAY53624 standard; protein; 373 AA 97US-0068958P. 98US-0101603P. 98US-0102540P. 98WO-US027008. (first entry) WPI; 2000-038344/03. CORP. N-PSDB; AAZ36230. (CHIR ) CHIRON Cao L; Homo sapiens. WO9933979-A2 18-DEC-1998; 24-SEP-1998; 30-DEC-1997; 22-FEB-2000 08-JUL-1999. Lin H, AAY53624 

```
be used to support colony forming cells or factor-dependent cell lines, to regulate hematopoiesis, and to treat myeloid or lymphoid cell deficiencies. In addition, they may be used to support the growth and proliferation of myeloid cells and confideration of erythroid progenitor cells, and to treat various anaemias. They can have colony stimulating factor (CSF) activity and can be used to support the growth and proliferation of myeloid cells such as granulocytes, monocytes or macrophages, to prevent or treat myelo: suppression, to support the growth and proliferation of megakaryocytes and platelets, thereby allowing prevention or treatment of platelet disorders such as thrombocytopenia, to support the growth and proliferation of hematopoeitic stem cells, either in place of or in conjunction with platelet transfusions, to treat stem cell disorders, such as aplastic anaemia and paroxysmal nocturnal hemoglobinuria, or to repopulate the stem cell compartment after irradiation or chemotherapy. They can be used for growth or differentiation of bone, cartilage, tendon, ligament, or nerve tissue, as well as for wound healing and tissue repair and replacement, and in the treatment of burns, incisions and ulcers, to induce cartilage and/or bone growth in circumstances where bone is not normally formed and thus have an application in healing bone fractures and cartilage and thus have an application in healing bone fractures and cartilage where prophylactic use in fracture creduction and also in the improved fixation of artificial joints
 120
 120
 SPLSAAAVSPSKLPEDDEPPARPPPPPASVSPQAEPVWTPPAPAAPAAPPSTS----- 173
 9
 9
 SPLSAAAVSPSKLPEDDEPPARPPPPPASVSPQAEPVWTPPAPAAPPATPAPRRRG
 AGLSAAPVPTAPAAGAPLMDFGNDFVPPAPRGPLPAAPPVAPERQPSWDPSPVSSTVPAP
 AGLSAAPVPTAPAAGAPLMDFGNDFVPPAPRGPLPAAPPVAPERQPSWDPSPVSSTVPAP
 1 MEDLDQSPLVSSSDSPPRPQPAFKYQFVREPEDEEEEEEEEEEDEDEDLEELEVLERKPA
 1 MEDLDQSPLVSSSDSPPRPQPAFKYQFVREPEDEEEEEEEEEEEDEDLEELEVLERKPA
 Gaps
 12;
 99.1%; Score 1833.8; DB 3; Length 373; 96.5%; Pred. No. 9.7e-65; ive 0; Mismatches 1; Indels 12;
 Matches 360; Conservative
 Local Similarity
 Sequence 373 AA;
 121
 셤
 g
 ò
 ò
```

```
1 MEDLDQSPLVSSSDSPPRPQPAFKYQFVREPEDEBEBEBEBEBEBEBEBEBEBEBELBVLBRKPA
 61 AGLSAAPVPTAPAAGAPLMDFGNDFVPPAPRGPLPAAPPVAPERQPSWDPSPVSSTVPAP
Query Match
Best Local Similarity 96.5
Matches 360; Conservative
 염
 셤
 ò
 셤
 ò
 ò
 228
 240
 288
 348
 KFAVLMWVFTYVGALFNGLTLLILALISLFSVPVIYERHQAQIDHYLGLANKOVKDAMAK 360
 VIQAIQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDSL 300
 ----VVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKG
 181 SSGSVVVDLLYWRDIKKTGVVFGASLFLLSLTVFSIVSVTAYIALALLSVTISFRIYKG
 VIQAIQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDSL
 KFAVLMWVFTYVGALFNGLTLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAK
 301
 349
 229
 241
 174
 289
```

ò 임 à 셤

1;

Gaps

12;

DB 3; Length 373; 1; Indels

99.1%; Score 1833.8; DB : 96.5%; Pred. No. 9.7e-65; ive 0; Mismatches 1

9 9

AGLSAAPVPTAPAAGAPLMDFGNDFVPPAPRGPLPAAPPAPAPERQPSWDSSTVPAP

MEDLDQSPLVSSSDSPPRPQPAFKYQFVREPEDEEEEEEEEEEBDEDEDLEELEVLERKPA

neurcendocrine-specific protein. The MAGI protein can be expressed by standard recombinant methodology. The MAGI polypeptides, polynucleotides and antibodies are useful for treating diseases, including neuropathies, spinal injury, neuronal degeneration, neuromuscular disorders, psychiatric disorders and developmental disorders, cancer, stroke and inflammatory disorders. The polynucleoitde is also useful for chromosome localization and for tissue expression studies. The present sequence

represents the human MAGI protein variant

Sequence 373 AA;

The invention relates to human MAGI protein, which is similar to

Claim 2; Page 22; 35pp; English

Novel polypeptides related to neuroendocrine-specific proteins ar polynucleotides useful for diagnosis of various diseases and for treatment of cancer and neurological disorders.

(SMIK ) SMITHKLINE BEECHAM PLC

Michalovich D,

N-PSDB; AAZ56888

99GB-00016898

19-JUL-1999;

99WO-GB002360.

WO200005364-A1

```
SPLSAAAVSPSKLPEDDEPPARPPPPPASVSPQAEPVWTPPAPAPAAPPSTS----- 173
 241 VIQAIQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDSL
 174 -----VVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKG
 KFAVLMWVFTYVGALFNGLTLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAK
 VIQAIQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDSL
 349 IQAKIPGLKRKAE 361
 229
 583
 g
 ò
```

AAB24242 ID AAB2 XX AC AAB2

MAGI protein; neuroendocrine-specific protein; neuropathy; human; spinal injury; neuronal degeneration; neuromscular disorder; cancer; psychiatric disorder; developmental disorder; inflammatory disorder; stroke; oytostatic; cerebroprotective; neuroprotective; variant.

Homo sapiens

Human MAGI polypeptide variant. 25-APR-2000 (first entry)

standard; protein; 373 AA.

AAY56969;

AAY56969

RESULT 2

g

Š

ò

AAB24242 standard; protein; 373 AA.

AAB24242

```
The present sequence is that of human NOGO-B. NOGO-B is a previously known splice variant of the human NOGO gene on chromosome 2p21. The invention relates to a novel splice variant, NOGO-C (see ABB82348). It provides NOGO-C polypeptides and polynucleotides, and methods for producing such polypeptides by recombinant techniques. Also disclosed are methods for utilising NOGO-C polypeptides and polynucleotides in the treatment of diseases including neuropathies, spinal injury, brain injury, stroke, neuronal degeneration, for example Alzheimer's disease and Parkinson's disease, neuromuscular disorders, psychiatric disorders and developmental disorders. Also provided are methods for identifying agonists and agonists for use in treating conditions associated with NOGO-C imbalance, and diagnostic assays for detecting diseases associated with inappropriate NOGO-C activity or levels
 KFAVLMWVFTYVGALFNGLTLLILALISLFSVPVIYERHQAQIDHYLGLANKOVKDAMAK 360
 NOGO-B; human; chromosome 2p21; neuropathy; spinal injury; brain injury; stroke; neuronal degeneration; Alzheimer's disease; Parkinson's disease; neuromuscular disorder; psychiatric disorder; developmental disorder; neuroprotective; nootropic; neuroleptic; antiparkinsonian; cerebroprotective; neuroleptic; diagnosis; therapy.
 New polypeptide designated NOGO-C is a splice variant of the human NOGO gene and may be useful in the treatment of neural disorders including Alzheimer's and Parkinson's diseases.
 1 MEDLDQSPLVSSSDSPPRPQPAFKYQFVREPEDEEEEEEEEEEDEDLEELEVLERKPA
 12; Gaps
 DB 4; Length 373;
 99.1%; Score 1833.8; DB 4; Length 96.5%; Pred. No. 9.7e-65; ive 0; Mismatches 1; Indels
 Disclosure; Page 27-38; 25pp; English.
 AAB82350 standard; protein; 373 AA
 (SMIK) SMITHKLINE BEECHAM PLC.
 24-JAN-2000; 2000GB-00001550.
 14-NOV-2000; 2000WO-GB004345.
 349 IQAKIPGLKRKAE 361
 (first entry)
 Best Local Similarity 96.:
Matches 360; Conservative
 Michalovich D, Prinjha
 361 IQAKIPGLKRKAE
 Human NOGO-B protein.
 WPI; 2001-343822/36.
 Similarity
 N-PSDB; AAF90325
 Sequence 373 AA;
 Homo sapiens.
 15-NOV-1999;
 23-JUL-2001
 25-MAY-2001.
 AAB82350;
 289
 301
 Query Match
 셤
 ò
 g
 8
 셤
 The present sequence represents a human stress-phosphorylated endoplasmic reticulum protein, designated Nogo B. Nogo B has cytostatic activity and is a modulator of the storage and acchange of calcium, cell growth and cellular stress response. It can: regulate oxidative stress; inhibit neurite outgrowth, neuron growth and axon regeneration. Nogo B polypeptides and polymucleotides are useful for anchilating stress levels and cellular stress response, cell growth and viability, diagnosis and treatment of cancer, malignant growth and other Nogo B related diseases. Nogo B polypeptides are also useful to screen combinatorial libraries to identify agonist or antagonist. Antibodies against Nogo B polypeptides are useful for affinity chromatography and distinguishing Nogo B
 AGLSAAPVPTAPAAGAPIMDFGNDFVPPAPRGPLPAAPPVAPERQPSWDPSPVSSTVPAP 120
 61 AGLSAAPVPTAPAAGAPLMDFGNDFVPPAPRGPLPAAPPVAPERQPSWDSSTVSSTVPAP 120
 121 SPLSAAAVSPSKLPEDDEPPARPPPPPASVSPQAEPVWTPPAPAPAPPSTS----- 173
 121 SPLSAAAVSPSKUPEDDEPPARPPPPPASVSPQAEPVWTPPAPAAPPAPPAPFRRG 180
 174 ----VVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKG 228
 240
 229 VIQAIQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDSL 288
 241 VIQAIQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDSL 300
 Novel protein associated with cell stress response useful for modulating stress levels, cell growth, diagnosis and treatment of cancer and malignant growth and for identifying agonists and antagonists.
 9
 9
 Human; Nogo B; cell stress response; hyperphosphorylated; brain tumour; stress-phosphorylated endoplasmic reticulum protein; cytostatic; gene therapy; cell growth; cellular stress response; neuron growth; regulator of oxidative stress; inhibitor of neurite outgrowth; axon regeneration; diagnosis; cancer; identification.
 1 MEDLIQQSPLVSSSDSPPRPQPAFKYQFVREPEDEEEEEEEEEEBDBDEDLEELEVLERKPA
 1 MEDLDQSPLVSSSDSPPRPQPAFKYQFVREPEDEEEEEEEEEEDEDEDLEELEVLERKPA
 Gaps
 12;
 DB 3; Length 373;
 1; Indels
 Score 1833.8; DB :
Pred. No. 9.7e-65;
 0; Mismatches
 Human Nogo B protein sequence SEQ ID NO:2.
 Williams LT;
 Claim 11; Fig 1A; 68pp; English.
 07-APR-2000; 2000WO-US009383
 08-APR-1999; 99US-0128372P.
21-JUN-1999; 99US-0140331P.
 99.1%;
96.5%;
(first entry)
 Matches 360; Conservative
 Wei D, Halenbeck R,
 WPI; 2000-665007/64.
 (CHIR) CHIRON CORP.
 Local Similarity
 N-PSDB; AAC64406.
 Sequence 373 AA;
 WO200060083-A1.
 Homo sapiens
 polypeptides
 12-OCT-2000
 61
 Query Match
```

셤 ሯ 셤 ð 셤 ઠે 셤 8

9 9 9

300

360

```
121 SPLSAAAVSPSKLPEDDEPPARPPPPPASVSPQAEFVWTPPAPAAPAAPSTFAAPKRRG 180
 289 KFAVLMWVFTYVGALFNGLTLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAK 348
 301 KFAVLMMVFTYVGALFNGLTLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAK
1 MEDLDQSPLVSSSDSPPRPQPAFKYQFVREPEDEBEEEEEEEDEDEDLEELEVLERKPA
 SPLSAAAVSPSKLPEDDEPPARPPPPASVSPQAEPVWTPPAPAAPPAPSTS-----
 VIQAIQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNCTIKELRRFFLVDDLVDSL
 ----VVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKG
 349 IQAKIPGLKRKAE 361
 WPI; 2002-627435/67.
N-PSDB; ABV94681.
 (CORI-) CORIXA CORP.
 cytostatic; tumour
 WO200260317-A2
 Homo sapiens.
 21-MAR-2001;
28-APR-2001;
 31-JAN-2001;
 14-JAN-2003
 08-AUG-2002
 229
 61
 174
 · w
 RESULT 6
 요
 셤
 a
D
 à
 à
 8
 ð
 ò
 The invention relates to human RTN4B protein and coding sequence, useful for providing a cDNA sequence of human RTN4B. The protein is an isomer of RTN4 with RTN family members. The present invention also refers to polypeptide encoded by a nucleotide sequence and manufacturing method and application of the polypeptide and polynucleotide
 173
 228
 240
 288
 241 VIQAIQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNCTIKELRRLFLFVDDLVDSL 300
 348
 AGLSAAPVPTAPAAGAPLMDFGNDFVPPAPRGPLPAAPPVAPERQPSWDSSTVPAP 120
 AGLSAAPVPTAPAAGAPLMDFGNDFVPPAPRGPLPAAPPVAPERQPSWDPSPVSSTVPAP
 SPLSAAAVSPSKLPEDDEPPARPPPPPASVSPQAEPVWTPPAPAPAAPPSTS-----
 ----VVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKG
 SSGSVVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKG
 KFAVLMWVFTYVGALFNGLTLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAK
 VIQAIQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDSL
 DB 5; Length 373;
 Human RTN 4B protein and coding sequence, its preparation and
 Score 1833.8; DB Pred. No. 9.7e-65; 0; Mismatches 1
 Claim 5; Page 11 (Disclosure); 27pp; Chinese
 AAM47954 standard; protein; 373 AA.
 tch 99.1%; al Similarity 96.5%; 360; Conservative (
 02-MAR-2000; 2000CN-00111791
 02-MAR-2000; 2000CN-00111791
 IQAKIPGLKRKAE 361
 361 İQAKİPGLKRKAE 373
 (first entry)
 õ
 Fu Q, Zhao Y;
 WPI; 2002-049934/07.
N-PSDB; ABA05903.
 Human RTN4B SEQ ID
 (UYFU-) UNIV FUDAN.
 Query Match
Best Local Similarity
 Sequence 373 AA
 Homo sapiens.
 Human; RTN4B
 CN1311439-A.
 04-MAR-2002
 05-SEP-2001
 121
 174
 181
 301
 61
 289
 349
 AAM47954;
 121
 229
 Yu L,
 RESULT
 g
 g
 셤
 à
 a
 ò
 d
 원
 à
 ò
 ð
```

```
The invention relates to an isolated polynucleotide (I) comprising: (a) any of a group of over 4000 nucleotide sequences (ABV94628-ABV99145); (b)
 New isolated polynucleotide and pancreatic tumor polypeptides, useful f
diagnosing, preventing and/or treating cancer, particularly pancreatic
 χ;
 Jiang
 pancreas; cancer; gene therapy; vaccine; immunostimulant;
 Hepler WT,
 Claim 2; SEQ ID NO 72; 300pp + Sequence Listing; English
 Human pancreatic cancer expressed protein SEQ ID NO 72.
 Lodes MJ, Persing DH,
 ABP68601 standard; protein; 373 AA
 2001US-0265305P.
2001US-0265682P.
2001US-0267568P.
2001US-0278651P.
2001US-0287112P.
 16-MAY-2001; 2001US-0291631P.
12-JUL-2001; 2001US-0305484P.
20-AUG-2001; 2001US-0313999P.
27-NOV-2001; 2001US-0333626P.
 30-JAN-2002; 2002WO-US002781
361 IQAKIPGLKRKAE 373
 (first entry)
 Benson DR, Kalos MD,
```

9

12;

1; Indels

Best Loca Matches

à

MEDLDQSPLVSSSDSPPRPQPAFKYQFVREPEDEBEBEBEBEBEBEDEDEDLBELEVLERKPA

```
complements of (a); (c) sequences consisting of at least 20 contiguous residues of (a); (d) sequences that hybridize to (a), under moderately stringent conditions; (e) sequences having at least 75% or 90% identity to (a); or (f) degenerate variants of (a). Polypeptides (ABP66596-fin a patient and compositions omprishing polypeptides (ABP66596-fin a patient and compositions comprishing polypeptides, polymolecides, antibodies, fusion proteins, T cell populations and antigen presenting an immune response. The polymolecides cancer and simulating an immune response. The polymolecides can be used as probes or primers for mucleic acid hybridisation, in the design and properties and proteins in the tumour cells, in vaccines and for gene therapy. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from NIPO at ftp.wipo.int/pub/published_pot_sequences
 120
 AGLSAAPVPTAPAAGAPLMDFGNDFVPPAPRGPLPAAPPVAPERQPSWDPSPVSSTVPAP 120
 173
 SPLSAAAVSPSKLPEDDEPPARPPPPPASVSPQAEPVWTPPAPAAPPSTPAAPKRRG 180
 228
 240
 VIQAIQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDSL 288
 KFAVLMWVFTYVGALFNGLTLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAK 348
 Nerve regeneration; neuroprotection; neuronal degeneration; CNS; PNS; central nervous system; peripheral nervous system; tranquillizer; Nogo; vulnerary; cerebroprotective; anti-tumour; antidiabetic; anticonvulsant; nootropic; antiparkinsonian; ophthalmological; analgesic; hepatotropic; osteopathic; vasotropic; nephrotropic; cytostatic; antigen; gene therapy; neurotransmitter receptor; human; receptor.
 60
 AGLSAAPVPTAPAAGAPLMDFGNDFVPPAPRGPLPAAPPVAPERQPSWDPSPVSSTVPAP
 SSGSVVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKG
 241 VIQAIQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDSL
 SPLSAAAVSPSKLPEDDEPPARPPPASVSPQAEPVWTPPAPAPAPPSTS-----
 ----VVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKG
 MEDLDQSPLVSSSDSPPRPQPAFKYQFVREPEDEEEEEEEEEDEDEDLEELEVLERKPA
 Gaps
 1; Indels 12;
 DB 5; Length 373;
 Score 1833.8; DB :
Pred. No. 9.7e-65;
0; Mismatches 1;
 Human neurotransmitter receptor protein Nogo-B.
 ABB81079 standard; protein; 373 AA
 99.18;
 IQAKIPGLKRKAE 361
 IOAKI PGLKRKAE 373
 Matches 360; Conservative
 Local Similarity
 Sequence 373 AA;
 US2002072493-A1
 Homo sapiens
 05-NOV-2002
 ABB81079;
 61
 61
 121
 174
 181
 229
 289
 301
 349
 361
 Query Match
 RESULT 7
 $$$$$$$$$$$$$$$$$$$$$$
 g
 ઠે
 g
 Š
 g
 Š
 g
 ò
 g
 ઠે
 유
 ò
 원
 ò
```

13-JUN-2002.

```
recording the control of preventing or inhibiting neuronal degeneration in the invention transfer to promote the central/peripheral nervous system (NS). The method involves administering NS-specific antigen, its analogue or its peptide, a nucleotide sequence the NS-specific antigen, its analogue or its peptide, a nucleotide sequence the NS-specific antigen or its analogue or combinations. The method is useful for promoting nerve regeneration and preventing neuronal degeneration in central/peripheral nervous system from injury/disease, where the injury is spinal cord injury, blunt from injury/disease, where the injury is spinal cord injury, blunt camages caused by surgery such as tumour excision. The disease is not an autoimmune disease or neoplasm. The disease results in a degenerative camages caused by surgery such as tumour excision. The disease is not an autoimmune disease or neoplasm. The disease results in a degenerative care process occurring in either gray or white matter or both. The disease is calcader neuropathy, senile dementia, Allzeimer's disease, barkinson's disease, facial nerve (Bell's) palsy, glaucoma, Huntington's chorea, anyotrophic lateral sclerosis, non-arteritic optic neuropathy, and vitamine deficiency, intervertebral dise heriation, peripheral care carpal tunnel syndrome, peripheral care carpal tunnel syndrome, peripheral care carpal tunnel syndrome, peripheral care incropathy, billary cirrhosis, primary anyoidosis, obstructive lung diseases, acromegaly, malabsorption caraxic neuropathy, billary cirrhosis, primary anyoidosis, obstructive lung diseases, acromegaly, malabsorption caraxic neuropathy, charical caraxic neuropathy, shillary cirrhosis, pathies, complications of various durgs (e.g., metronidazole) and toxins (e.g., alcohol or organophosphates), Charcot-Marie-Tooth disease, ataxia, anyloid polyneuropathie, caraxia, anyloid polyneuropathy, diant axonal neuropathy, and disease, or lipoproteinemia. The present sequence represents the human controlled.
 61 AGLSAAPVPTAPAAGAPLMDFGNDFVPPAPRGPLPAAPPVAPERQPSWDPSPVSSTVPAP 120
 9
 1 MEDLIQOSPLVSSSDSPPRPQPAFKYQFVREPEDEBEBEBEBEBEBBBBDLBBLBVLBRRPA
 SPLSAAAVSPSKLPEDDEPPARPPPPPASVSPQAEPVWTPPAPAPAAPPSTS-----
 ----VUDLLYWRDIKKTGVVPGASLPLLSLTUFSIVSVTAYIALALLSVTISFRIYKG
 1 MEDLDQSPLVSSSDSPPRPQPAFKYQFVREPEDEEEEEEEEEEBDBDLEELEVLERKPA
 Mosonego A;
 Promoting nerve regeneration and preventing neuronal degeneration in central/peripheral nervous system from injury/disease, comprises administering nervous system-specific activated T cells/antigen, or
 The invention relates to promoting nerve regeneration or conferring
 1.8; DB 5; Length 373;
9.7e-65;
 Beserman P,
 Cohen IR,
 99.1%; Score 1833.8;
96.5%; Pred. No. 9.7e-
ive 0; Mismatches
 Example; Page 56-57; 93pp; English.
 Hauben E,
 98ND-00124500.
98WO-US014715.
98US-00218277.
99US-00314161.
 CO LTD
 2001US-00893348,
 Best Local Similarity
Matches 360; Conservative
 RES & DEV
 Eisenbach-Schwartz M,
 WPI; 2002-607255/65.
N-PSDB; ABN86601.
 Similarity
 analogs/peptides.
 Sequence 373 AA;
 21-JUL-1998;
22-DEC-1998;
19-MAY-1999;
 28-JUN-2001;
 (YEDA) YEDA
 19-MAY-1998;
 Moalem G;
 174
 61
 Query Match
셤
 ; ∂
 g
 셤
 ઠ
```

φ

```
289
 61
 121
 ADK67503;
 61
 Query Match
 Yan R,
 ADK67503
 8x3633
 셤
 용
 ð
 셤
 ద
 셤
 ઠે
 ò
 ò
 ð
 à
 ò
 셤
 This invention describes novel nucleic acid molecules that are associated with apoptosis and encode a polypeptide and are derived from a normalised gene library (embryonic or liver) or clone collections, and the extent of apoptosis measured by cell death detection assay or the CPRG assay (measuring loss of membrane integrity). The products of the invention have extostatic, neuroprotective, immunosuppressive, antitheumatic, on antiarthritic, dermatological, antiinflammatory, hepatotropic, virucide, notropic, anticonvulsant, antiparkinsonian, vasotropic, cerebroprotective and antialcoholic activity and can be used for gene therapy. The polynucleotides also related vectors, hosts (or their cerebroprotective and antialcoholic activity and can be used for therapy. The polynucleotides also related vectors, nosts (or their cerebroprotective and antialcoholic activity and can be used for treatment or prevention of tumours, autoimmune or desenerative diseases and viral infections, specifically leukamia, carcinoma, sarcoma, multiple sclerosis, rheumatoid arthritis, diabetes, lupus, or infection
SSGSVVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKG 240
 348
 nucleic acids involved in apoptosis, useful for diagnosis and then the e.g. tumors and degenerative disease, also related proteins,
 antirheumatic; antiarthritic, dermatological; antiinflammatory; hepatotropic; virucide; nootropic; antiachrismatic; antiparkinsonian; vasotropic; cerebroprotective; antialcoholic; gene therapy; tumour; autoimmune disease; degenerative disease; viral infection; leukaemia; carcinoma; sarcoma; multiple solerosis; rheumatoid arthritis; diabetes; lupus; hepatitis; influenza viruses; Alzheimer's disease; Huntington's disease; Parkinson's disease; reperfusion injury; stroke;
 apoptosis; cell death; cytostatic; neuroprotective; immunosuppressive;
 KFAVLMWVFTYVGALFNGLTLLILALISLFSVPVIYBRHQAQIDHYLGLANKNVKDAMAK
 multiple sclerosis, rheumatoid arthritis, diabeces, ingue, or inc. with hepatitis or influenza viruses, Alzheimer's, Huntington's or
 Kesper B;
 Human apoptosis-associated protein SEQ ID 487.
 Schaefer R,
 Claim 1b; SEQ ID NO 487; 517pp; German.
 ADI63044 standard; protein; 373 AA.
 Kazinski M,
 alcoholic liver disease; human
 (XANT-) XANTOS BIOMEDICINE AG
 13-JAN-2003; 2003WO-EP000270.
 11-JAN-2002; 2002DE-01000856.
 IOAKIPGLKRKAE 361
 treatment of e.g. tumors a antibodies and modulators.
 22-APR-2004 (first entry)
 WPI; 2003-542134/51.
 Koenig-Hoffman K,
 WO2003058021-A2
 Homo sapiens
 17-JUL-2003.
 181
 301
 349
 361
 ADI63044;
 229
 289
 ద
 엄
 d
 ò
 g
 à
 ઠે
```

```
Parkinson's diseases, reperfusion injury, stroke and alcoholic liver disease. Detection of the polymucleotides and derived polypeptides can also be used for diagnosis of these diseases. This sequence represents an apoptosis-associated protein described in the invention.
 120
 120
 173
 348
 9
 9
 New polypeptide having BACE1 activity, useful in preparing a composition for treating amyloidosis or Alzheimer's disease.
 neuroprotective; gene therapy; BACE1 activity; RTN4; RTN3; amyloidosis;
Alzheimer's disease.
 181 SSGSVVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSSTAAYAYIALALLSVTISFRIYKG
 AGLSAAPVPTAPAAGAPLMDFGNDFVPPAPRGPLPAAPPVAPERQPSWDPSPVSSTVPAP
 SPLSAAAVSPSKLPEDDEPPARPPPPASVSPQAEPVWTPPAPAPAPASTS-----
 KFAVLMWVFTYVGALFNGLTLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAK
 1 MEDLDQSPLVSSSDSPPRPQPAFKYQFVREPEDEBEEEEEEEEBEDEDLEELEVLERKPA
 174 -----VVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKG
 VIQAIQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDSL
 Gaps
 12;
 99.1%; Score 1833.8; DB 7; Length 373; 96.5%; Pred. No. 9.7e-65; ive 0; Mismatches 1; Indels 12;
 Claim 52; SEQ ID NO 8; 42pp; English.
 ADK67503 standard; protein; 373 AA.
 (PHAA) PHARMACIA & UPJOHN CO
 17-APR-2002; 2002US-0373284P.
 08-APR-2003; 2003WO-US008829.
 349 IQAKIPGLKRKAE 361
 (first entry)
 Best Local Similarity 96.5
Matches 360; Conservative
 361 IQAKIPGLKRKAE
 Human RTN-4B protein.
 WPI; 2003-854033/79.
 Sequence 373 AA;
 WO2003088926-A2.
 Homo sapiens.
 06-MAY-2004
 30-OCT-2003.
 걐
```

```
sapiens
 21-OCT-2002
 289
 349
 ABG30937;
 61
 121
 229
 Peptide
 Homo
 RESULT 11
 ABG30937
 ઠે
 셤
 δ
 名
 ò
 셤
 δ
 셤
 ઠે
 ద
 Š
 셤
 ò
 셤
 AGLSAAPVPTAPAAGAPLMDFGNDFVPPAPRGPLPAAPPVAPERQPSWDPSPVSSTVPAP 120
 61 AGLSAAPVPTAPAAGAPLMDFGNDFVPPAPRGPLPAAPPVAPERQPSWDPSPVSSTVPAP 120
 121 SPLSAAAVSPSKLPEDDEPPARPPPPASVSPQAEPVWTPPAPAPAPPSTS----- 173
 -----VVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKG 228
 181 SSGSVVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKG 240
 VIQAIQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDSL 288
 241 VIQAIQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDSL 300
 KFAVLMWVFTYVGALFNGLTLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAK 348
 301 KFAVLMMVFTYVGALFNGLTLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAK 360
 9
 9
 The invention relates to an isolated polypeptide having BACE1 activity. The protein is RTN4 or RTN3 protein. The polypeptide is useful in preparing a composition for treating amyloidosis or Alzheimer's disease. This sequence corresponds to the RTN-4B protein.
 1 MEDLDQSPLVSSSDSPPRPQPAFKYQFVREPEDEEEEEEEEEEDEDEDLEELEVLERKPA
 MEDLDQSPLVSSSDSPPRPQPAFKYQFVREPEDEEEEEEEEEEEDEDDLEELEVLERKPA
 contactin~associated protein-1; Caspr; neuroprotective; gene therapy; CNS; spinal cord injury; multiple sclerosis; epilepsy; stroke.
 Gaps
 12;
 DB 7; Length 373;
 1; Indels
 human; Nogo-B; neurite outgrowth inhibitor; Nogo;
 Score 1833.8; DB 7
Pred. No. 9.7e-65;
0; Mismatches 1;
 PTE LTD.
 Ä
 373
 GEN HOSPITAL
R.
 99.1%;
 05-DEC-2003; 2003WO-GB005329
 06-DEC-2002; 2002US-0431549P
20-JUN-2003; 2003US-0480138P
 standard; protein;
 IQAKIPGLKRKAE 361
 (first entry)
 Matches 360; Conservative
 Human Nogo-B protein.
 WPI; 2004-468705/44
 SINGAPORE (
 Best Local Similarity
 Sequence 373 AA;
 WO2004052389-A2.
 09-SEP-2004
 Homo sapiens
 24-JUN-2004
 229
 349
 61
 289
 ADP67235
 174
 ADP67235
 Query Match
 (SIGE-)
 (FORR/)
 Xiao Z;
 X8888XX
 ò
 g
 ઠે
 셤
 ઠે
 g
 ઠે
 셤
 Š
 셤
 ઠ
 g
 ઠે
 g
```

```
ä
 300
 The invention relates to a novel composition comprising neurite outgrowth inhibitor (Nogo) and contactin-associated protein-1 (Caspr) or its mimetics or a substance capable of promoting interaction between Nogo and Caspr, in combination with a carrier. A composition of the invention has neuroprotective activity, and may have a use in gene therapy. The composition is useful for treating injury to or disease of the CNS, e.g. spinal cord injury, multiple sclerosis, epilepsy or stroke. The present sequence represents human Nogo-B.
 180
 228
 240
 288
 348
 301 KFAVLMMVFTYVGALFNGLTLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAK 360
 61 AGLSAAPVPTAPAAGAPLMDFGNDFVPPAPRGPLPAAPPVAPERQPSWDPSPVSSTVPAP 120
 AGLSAAPVPTAPAAGAPLMDFGNDFVPPARGPLPAAPPVAPERQPSWDPSPVSSTVPAP 120
 9
New composition comprising Nogo and Caspr or a substance capable of promoting interaction between Nogo and Caspr useful for treating injury to or disease of the CNS, e.g., spinal cord injury, multiple sclerosis,
 Human; Nogo; BACE; acute neuronal injury; spinal injury; head injury; stroke; peripheral nerve damage; neoplastic disorder; glioblastoma; neuroblastoma; hyperproliferative disorder; dysproliferative disorder; cirrhosis; psoriasis; keloid formation; fibrocystic condition; cancer; tissue hypertrophy; central nervous system; axon regeneration; NogoB;
 SPLSAAAVSPSKLPEDDEPPARPPPPPASVSPQAEPVWTPPAPAPAPAPFKRRG
 181 SSGSVVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYJALALLSVTFFKKG
 1 MEDLIDQSPLVSSSDSPPRPQPAFKYQFVREPEDEEEEEEEEEEEEEEEEEEEELEVLERKPA
 SPLSAAAVSPSKLPEDDEPPARPPPPPASVSPQAEPVWTPPAPAPAPAPFSTS-----
 174 ----VVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKG
 VIQAIQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDSL
 241 VIQAIQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDSL
 KFAVLMWVFTYVGALFNGLTLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAK
 MEDLDQSPLVSSSDSPPRPQPAFKYQFVREPEDEBEEEEEEEBDBDBDLBBLEVLERKPA
 Gaps
 12;
 Length 373;
 Indels
 DB 8;
 99.1%; Score 1833.8; DB (96.5%; Pred. No. 9.7e-65; iive 0; Mismatches 1
 92. .104
/note= "NogoB (ASY) peptide"
 Disclosure; Page 14; 202pp; English.
 Nogo-associated disease; metastasis
 Location/Qualifiers
 Ą
 373
 ABG30937 standard; protein;
 IQAKIPGLKRKAE 361
 entry)
 Matches 360; Conservative
 Human NogoB protein.
 (first
 epilepsy or stroke.
 Query Match
Best Local Similarity
 Sequence 373 AA;
```

300

```
301 KFAVLMMVFTYVGALFNGLTLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAK 360
 KFAVLMWVFTYVGALFNGLTLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAK 348
 61 AGLSAAPVPTAPAAGAPLMDFGNDFVPPAPRGPLPAAPPVAPERQPSWDPSPVSSTVPAP 120
 neuroendocrine specific protein. The MAGI protein can be expressed by standard recombinant methodology. The MAGI polypeptides, polynucleotides and antibodies are useful for treating diseases, including neuropathies, spinal injury, neuronal degeneration, neuromuscular disorders, psychiatric disorders and developmental disorders, cancer, stroke and inflammancy disorders. The polynucleoitde is also useful for chromosome localization and for tissue expression studies. The present sequence represents the human MAGI protein
 241 VIQAIQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDSL
 1 MEDLIDQSPLVSSSDSPPRPQPAFKYQFVREPEDEEEEEEEEEEEBEDEDELEELEVLERKPA
 229 VIQAIQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDSL
 MAGI protein; neuroendocrine-specific protein; neuropathy; human; spinal injury; neuronal degeneration; neuromuscular disorder; cancer; psychiatric disorder; developmental disorder; inflammatory disorder;
 1 MEDLDQSPLVSSSDSPPRPQPAFKYQFVREPEDEEEEEEEEEEDEDLEELEVLERKPA
 Novel polypeptides related to neuroendocrine-specific proteins and polynucleotides useful for diagnosis of various diseases and for treatment of cancer and neurological disorders.
 The invention relates to human MAGI protein, which is similar to
 DB 3; Length 1192;
 95.0%; Score 1756.9; DB 3; Length 30.3%; Pred. No. 8.5e-61; ive 0; Mismatches 0; Indels
 stroke; cytostatic; cerebroprotective; neuroprotective
 AAY56967 standard; protein; 1192 AA.
 Claim 2; Page 20-21; 35pp; English.
 (SMIK) SMITHKLINE BEECHAM PLC.
 99GB-00016898.
 99WO-GB002360
 98GB-00016024,
 Michalovich D, Prinjha RK;
 361 IQAKIPGLKRKAE 373
 IQAKIPGLKRKAE 361
 Conservative
 Human MAGI polypeptide.
 WPI; 2000-182693/16.
 Local Similarity
 Sequence 1192 AA;
 N-PSDB; AAZ56886.
 WO200005364-A1.
 Homo sapiens
 21-JUL-1999;
 22-JUL-1998;
 25-APR-2000
 19-JUL-1999;
 361;
 03-FEB-2000,
 289
 349
 Query Match
 Best Loca
Matches
 AAY56967
 g
 유
 g
 셤
 ઠે
 ઠે
 8
 8
 The present invention relates to a new method of identifying modulators of Nogo function or BACE activity. The method involves providing Nogo and BACE bulging with each other, monitoring the interaction between these polypeptides, and determining if the test agent is a modulator of Nogo or BACE activity. The method is useful in treating caute neuronal injuries, such as spinal or head injury, stroke, peripheral nerve damage, and in neoplastic (e.g. glioblastomas). Apperproliferative or dysproliferative disorders (e.g. inrhosis, psoriasis, keloid formation, fibrocystic conditions, tissue hypertrophy) of the central nervous system. The BACE polypeptide is useful in screening methods to identify agents that may act as modulators of BACE activity and in particular agents that may be useful in treating Nogo-associated diseases. The modulators of Nogo or BACE polypeptides, and the polynucleotide encoding the BACE polypeptide are useful in manufacturing a medicament for the treatment or prevention of disorders responsive to the modulation of Nogo activity, in alleviating the symptoms or improving the condition of a patient suffering from this disorder. The polynucleotide may also be an essential component in assays, a probe, in recombinant protein synthesis, and in gene therapy techniques. The present amino acid sequence represents the human NogoB
 AGLSAAPVPTAPAAGAPLMDFGNDFVPPAPRGPLPAAPPVAPERQPSWDPSPVSSTVPAP 120
 120
 173
 SSGSVVVDLLYWRDIKKTGVVFGASLFLLSLTVFSIVSVTAYIALALLSVTISFRIYKG 240
 9
 9
 Identifying modulators of Nogo or BACE activity for treating acute neuronal injuries, neoplastic or dysproliferative disorders, comprises providing and monitoring interaction between Nogo and BACE polypeptides.
 MEDLDQSPLVSSSDSPPRPQPAFKYQFVRBPEDEEEEEEEEBBDEDEDLEELEVLERKPA
 61 AGLSAAPVPTAPAAGAPLMDFGNDFVPPAPRGPLPAAPPVAPERQPCWDFSPVSSTVPAP
 1 MEDLDQSPLVSSSDSPPRPQPAFKYQFVREPEDEEEEEEEEEEDEDLEELEVLERKPA
 SPLSAAAVSPSKLPEDDEPPARPPPPPASVSPQAEPVWTPPAPAPAAPPSTS----
 SPLSAAAVSPSKLPQDDEPPARPPPPASVSPQAEPVWTPPAPAPPAPPSTPAAPKRRG
 ----VVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKG
 /note= "NogoB (ASY) peptide, distinguishes NogoB from other Nogo isoforms"
 Gaps
 12;
 Score 1825.8; DB 5; Length 373;
Pred. No. 2e-64;
1; Mismatches 2; Indels 12;
 Ä
 Blackstock WP, Hale RS, Prinjha R, Rowley
 /note= "NogoB (ASY) peptide"
 Example 1; Page 25; 68pp; English.
 (GLAX) GLAXO GROUP LTD.
(SMIK) SMITHKLINE BEECHAM PLC.
 98.7%;
96.0%;
 18-JAN-2002; 2002WO-GB000228.
 18-JAN-2001; 2001GB-00001312.
180. 193
 Matches 358; Conservative
 protein of the invention
 WPI; 2002-599722/64
 Local Similarity
 N-PSDB; ABK90133
 Seguence 373 AA;
 WO200257483-A2
 25-JUL-2002
 61
 121
 121
 174
 Query Match
Peptide
 Peptide
```

ä

ઠે 요 ò g ò g 8 임

9

| Db 1141 LILALISLESVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAKIPGLKRKAE 1192 | RESULT 13<br>AAB82349<br>ID AAB82349 standard; protein; 1192 AA. | XX<br>AC AAB82349; | XX<br>DT 23-JUL-2001 (first entry)<br>yy                             | DE Human NOGO-A protein. |                                                                  | KW neurogrotective; noofroje; psychiatric disorder; developmental disorder;<br>KW neurogrotective; noofroje; neuroleptic; antiparkinsonian;<br>KW cerebroorderive; neuroleptic, diamosie, therany |     |                                                                  | AX PD 25-MAY-2001. | PF 14-NOV-2000; 2000WO-GB004345.                                     | AA PR 15-NOV-1999; 99GB-00026995. PR 24-JAN-2000; 2000GB-00001550. | (SMIK ) SMITH                                                        | Michalo | wpt. 2001-242022/26                                                  |         | PT New polypeptide designated NOGO-C is a splice variant of the human NOGO PT cene and may be useful in the treatment of neural disorders including | Alzheimer's and | PS Disclosure; Page 26-27; 25pp; English.                            |         |                                                                      |         |                                                                      |         | CC agonists and agonists for use in tratting conditions associated with NOGO CC -C imbalance, and diagnostic assays for detecting diseases associated |         |                                                                      | 95.0%; Score 1756.9; DB nilarity 30.3%; Pred. No. 8.5e-61 | _                                                                     | OY 1 MEDLDQSPLVSSSDSPPRPQPAFKYQFVREPEDEEEEEEEEBEDEDLEELEVLERKPA 60  | Qy 61 AGLSAAPVPTAPAAGAPLMDFGNDFVPPAPRGPLPAAPPVAPERQPSWDPSPVSTVPAP 120 | 121 SPLSAAAVSPSKLPEDDEPPARPPPPASVSPQAEPVWTPPAPAPPRS          |
|-------------------------------------------------------------------|------------------------------------------------------------------|--------------------|----------------------------------------------------------------------|--------------------------|------------------------------------------------------------------|---------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|-----|------------------------------------------------------------------|--------------------|----------------------------------------------------------------------|--------------------------------------------------------------------|----------------------------------------------------------------------|---------|----------------------------------------------------------------------|---------|-----------------------------------------------------------------------------------------------------------------------------------------------------|-----------------|----------------------------------------------------------------------|---------|----------------------------------------------------------------------|---------|----------------------------------------------------------------------|---------|-------------------------------------------------------------------------------------------------------------------------------------------------------|---------|----------------------------------------------------------------------|-----------------------------------------------------------|-----------------------------------------------------------------------|---------------------------------------------------------------------|-----------------------------------------------------------------------|--------------------------------------------------------------|
|                                                                   | 121 SPLSAAAVSPSKLPEDDEPPARPPPPASVSPQAEPVWTPPAPAPAPPS 171         | 172 171            | 181 SSGSVDETLFALPAASEPVIRSSAENMDLKEQPGNTISAGQEDFPSVLLETAASLPSLSP 240 | 172 171                  | 241 LSAASFKEHEYLGNLSTVLPTEGTLQENVSEASKEVSEKAKTLLIDRDLTEFSELEYSEM | 201 GSSERVSDKARSAVTVANDBERTTVKNKHEREKT.VSNNTI.HNOOFI.DFAITWT.VKNERVV 260                                                                                                                          | 172 | 361 SSEKAKDSFNEKRVAVEAPMREEYADFKPFERVWEVKDSKEDSDMLAAGGKIESNLESKV | 172 171            | 421 DKKCFADSLEQTNHEKDSESSNDDTSFPSTPEGIKDRPGAYITCAPFNPAATESIATNIF 480 | 172 171                                                            | 481 PLLGDPTSENKTDEKKIEEKKAQIVTEKNTSTKTSNPFLVAAQDSETDYVTTDNLTKVTE 540 | 172 171 | 541 EVVANMPEGLIPDLVQEACESELNEVIGTKIAYETKMDLVQTSEVMQESLYPAAQLCPSF 600 | 172 171 | 601 EESEATPSPVLPDIVMEAPLNSAVPSAGASVIQPSSSPLEASSVNYESIKHEPENPPPYE 660                                                                                | 172 171         | 661 EAMSVSLKKVSGIKEEIKEPENINAALQETEAPYISIACDLIKETKLSAEPAPDFSDYSE 720 | 172 171 | 721 MAKVEQPVPDHSELVEDSSPDSEPVDLFSDDSIPDVPQKQDETVMLVKESLTETSFESMI 780 | 172 171 | 781 EYENKEKLSALPPEGGKPYLESFKLSLDNTKDTLLPDEVSTLSKKEKIPLQMEELSTAVY 840 | 172 171 | 841 SNDDLFISKEAQIRETETFSDSSPIEIIDEFPTLISSKTDSFSKLAREYTDLEVSHKSEI 900                                                                                  | 172 171 | 901 ANAPDGAGSLPCTELPHDLSLKNIQPKVBEKISFSDDFSKNGSATSKVLLLPPDVSALAT 960 | 172TSVVDLLYWRDIKKTGVV 189                                 | 961 QAEIBSIVKPKVLVKEAEKKLPSDTEKEDRSPSAIFSAELSKTSVVDLLYWRDIKKTGVV 1020 | 190 FGASLFLLSLTVFSIVSVTAVIALALLSVTISFRIYKGVIQAIQKSDEGHPFRAYLESE 249 | 250 VAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDSLKFAVLMWVFTYVGALFNGLTL 309  | 310 LILALISLESVPVIYERHQAQIDHYLGLANKNVKDANAKIQAKIPGLKKKAE 361 |
| අු                                                                | \$ A                                                             | ò                  | đ                                                                    | ò                        | qq                                                               | ð 5                                                                                                                                                                                               | 8 8 | . A                                                              | ò                  | g                                                                    | Š                                                                  | qq                                                                   | ò       | qq                                                                   | ò       | qq                                                                                                                                                  | ò               | a                                                                    | ò       | q                                                                    | ò       | g                                                                    | ò       | g                                                                                                                                                     | ò       | đ                                                                    | Š                                                         | g                                                                     | & A                                                                 | 8 8                                                                   | 8 8                                                          |

÷

| STULPTEGTLQE STULPTEGTLQE VANPREEIIVKNI VEAPMREEYADFI VEAPMREEYADFI COSESSINDTSFI KIEEKKAQIVTEI COSESSINEVT COSESSINEVT COSESSINEVT COSESSINEVT COSESSINEVT COSESSINEVT COSESSINEVT COSESSINEVT COSESSINEVT COSESSINEVT COSESSINEVT COSESSINEVT COSESSINEVT COSESSINEVT COSESSINEVT COSESSINEVT COSESSINEVT COSESSINEVT COSESSINEVT COSESSINEVT COSESSINEVT COSESSINEVT COSESSINEVT COSESSINEVT COSESSINEVT COSESSINEVT COSESSINEVT COSESSINE COSESSINE COSESSINE COSESSINE COSESSINE COSESSINE COSESSINE COSESSINE COSESSINE COSESSINE COSESSINE COSESSINE COSESSINE COSESSINE COSESSINE COSESSINE COSESSINE COSESSINE COSESSINE COSESSINE COSESSINE COSESSINE COSESSINE COSESSINE COSESSINE COSESSINE COSESSINE COSESSINE COSESSINE COSESSINE COSESSINE COSESSINE COSESSINE COSESSINE COSESSINE COSESSINE COSESSINE COSESSINE COSESSINE COSESSINE COSESSINE COSESSINE COSESSINE COSESSINE COSESSINE COSESSINE COSESSINE COSESSINE COSESSINE COSESSINE COSESSINE COSESSINE COSESSINE COSESSINE COSESSINE COSESSINE COSESSINE COSESSINE COSESSINE COSESSINE COSESSINE COSESSINE COSESSINE COSESSINE COSESSINE COSESSINE COSESSINE COSESSINE COSESSINE COSESSINE COSESSINE COSESSINE COSESSINE COSESSINE COSESSINE COSESSINE COSESSINE COSESSINE COSESSINE COSESSINE COSESSINE COSESSINE COSESSINE COSESSINE COSESSINE COSESSINE COSESSINE COSESSINE COSESSINE COSESSINE COSESSINE COSESSINE COSESSINE COSESSINE COSESSINE COSESSINE COSESSINE COSESSINE COSESSINE COSESSINE COSESSINE COSESSINE COSESSINE COSESSINE COSESSINE COSESSINE COSESSINE COSESSINE COSESSINE COSESSINE COSESSINE COSESSINE COSESSINE COSESSINE COSESSINE COSESSINE COSESSINE COSESSINE COSESSINE COSESSINE COSESSINE COSESSINE COSESSINE COSESSINE COSESSINE COSESSINE COSESSINE COSESSINE COSESSINE COSESSINE COSESSINE COSESSINE COSESSINE COSESSINE COSESSINE COSESSINE COSESSINE COSESSINE COSESSINE COSESSINE COSESSINE COSESSINE COSESSINE COSESSINE COSESSINE COSESSINE COSESSINE COSESSINE COSESSINE COSESSINE COSESSINE COSESSINE COSESSINE COSESSINE COSESSINE COSESSINE COSESSINE COSESSINE COSESSINE COSESSINE COSESSINE COSESSINE COSESS | TEGTLQENVSEASKEVSER TEGTLQENVSEASKEVSER TEITVKNKDEEEKLVSNNI TEETADFKPFERVWEVKDE TOTAL TERMINATER TELNEVTGTKIAYETKMDI TELNEVTGTKIAYETKMDI TELNEVTGTKIAYETKMDI TELNEVTGTKIAYETKMDI TELNEVTGTKIAYETKMDI TELNEVTGTKIAYETKMDI TELNEVTGTKIAYETKMDI TELNEVTGTKIAYETKMDI TELNEVTGTKIAYETKMDI TELNEVTGTKIAYETKMDI TELNEVTGTKIAYETKMDI TELNEVTGTKIAYETKMDI TELNEVTGTKIAYETTLEDEV TELNINAALQETEAPYISIAK TELNINAALQETEAPYISIAK TELNINAALQETEAPYISIAK TELNINAALGETEAPYISIAK TELNINAALGETEAPYISIAY TELNINAALGETEAPYISIAY TELNINAALGETEAPYISIAY TELNINAALGETEAPYISIAY TELNINAALGETEAPYISIAY TELNINAALGETEAPYISIAY TELNINAALGETEAPYISIAY TELNINAALGETEAPYISIAY TELNINAALGETEAPYISIAY TELNINAALGETEAPYISIAY TELNINAALGETEAPYISIAY TELNINAALGETEAPYISIAY TELNINAALGETEAPYISIAY TELNINAALGETEAPYISIAY TELNINAALGETEAPYISIAY TELNINAALGETEAPYISIAY TELNINAALGETEAPYISIAY TELNINAALGETEAPYISIAY TELNINAALGETEAPYISIAY TELNINAALGETEAPYISIAY TELNINAALGETEAPYISIAY TELNINAALGETEAPYISIAY TELNINAALGETEAPYISIAY TELNINAALGETEAPYISIAY TELNINAALGETEAPYISIAY TELNINAALGETEAPYISIAY TELNINAALGETEAPYISIAY TELNINAALGETEAPYISIAY TELNINAALGETEAPYISIAY TELNINAALGETEAPYISIAY TELNINAALGETEAPYISIAY TELNINAALGETEAPYISIAY TELNINAALGETEAPYISIAY TELNINAALGETEAPYISIAY TELNINAALGETEAPYISIAY TELNINAALGETEAPYISIAY TELNINAALGETEAPYISIAY TELNINAALGETEAPYISIAY TELNINAALGETEAPYISIAY TELNINAALGETEAPYISIAY TELNINAALGETEAPYISIAY TELNINAALGETEAPYISIAY TELNINAALGETEAPYISIAY TELNINAALGETEAPYISIAY TELNINAALGETEAPYISIAY TELNINAALGETEAPYISIAY TELNINAALGETEAPYISIAY TELNINAALGETEAPYISIAY TELNINAALGETEAPYISIAY TELNINAALGETEAPYISIAY TELNINAALGETEAPYISIAY TELNINAALGETEAPYISIAY TELNINAALGETEAPYISIAY TELNINAALGETEAPYISIAY TELNINAALGETEAPYISIAY TELNINAALGETEAPYISIAY TELNINAALGETEAPYISIAY TELNINAALGETEAPYISIAY TELNINAALGETEAPYISIAY TELNINAALGETEAPYISIAY TELNINAALGETEAPYISIAY TELNINAALGETEAPYISIAY TELNINAALGETEAPYISIAY TELNINAALGETEAPYISIAY TELNINAALGETEAPYISIAY TELNINAALGETEAPYISIAY TELNINAALGETEAPYISIAALAGETEAPYISIAY TELNINAALGETEAPYISIAY TELNINAALGETEAPYISIAY TELNINAALGETEAPYISIAY TELNINAALGETEAPYISIAY TELNINAALGETEAPYISIAY T | SSGSVDETLFALPAASEEVIRSSAENMDLKEQPGNTISAGGEDFPSVLLETAASLPSLSP LSAASFKEHEYLGNLSTVLPTEGTLQENVSEASKEVSEKAKTLLIDRDLTEFSELEYSEM GSSFSVSPKAESAVIVANPREEIIVKONEDEEKLVSNNILHNQQELPTALTKLVKEDEVV GSSEKAKDSFNEKRAVAVEAPMREEYADFKPFRYWEVKOSKEDSDMLAAGGKIESNLESKY  BLLGDPTSENKTDEKKIEEKKAQIVTEKATSTKISNPFLVAAQDSETDYVTTDNLTKVTE EVVANMPEGLTPDLVQEACESELNEVTGKIAYETKMDLVQTSEVMGESLYPBAQLCPSF ESSEATOSFNEKRYSGIKEEIKEPENINAALQETEAPYISIACDLIKETKLSAEPAPDFSDYS  ENASVSLKKVSGIKEEIKEPENINAALQETEAPYISIACDLIKETKLSAEPAPDFSDYSE  BAMSVELKYVSGIKEEIKEPENINAALQETEAPYISIACDLIKETKLSAEPAPDFSDYSE  BAMSVELKYVSGIKETETFSDSSPIEIIDEFPTLISSKTDSFSKLAREYTDLEVSHKSEI  SNDDLFISKEAQIRETETFSDSSPIEIIDEFPTLISSKTDSFSKLAREYTDLEVSHKSEI  SNDDLFISKEAQIRETETFSDSSPIEIIDEFPTLISSKTDSFSKLAREYTDLEVSHKKTOV |
|--------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|--------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|-----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
|--------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|--------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|-----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|

RESULT 14

```
The sequence is the human Nogo protein, a 250kDa myelin-associated axon growth inhibitor. The invention relates to the use of the nogo receptor, nogo protein, their nucleic acids, vectors expressing them and antibodies against them, to isolate agents which block nogo receptor mediated axonal growth. The agent is useful for treating a central nervous system disorder which is a result of cranial or cerebral trauma, spinal cord
 Human; Nogo receptor; axonal growth; immunogen; antibody; nogo protein; cranial trauma; cerebral trauma; spinal cord injury; stroke; demyelinating disease; multiple sclerosis; monophasis demyelination; encephalomyelitis; multifocal leukcencephalopathy; panencephalitis; multifocal leukcencephalopathy; panencephalitis; Marchiafava-Bignami disease; pontine myelinolysis; adrenoleukodystrophy; Canavan's disease; metachromatic leukodystrophy; viral infection; krabbe's disease.
 Novel Nogo receptor protein useful for identifying modulator of Nogo protein or Nogo receptor protein, which is useful for treating central nervous system disorders.
 Location/Qualifiers
1054. .119
/label= Lumenal_extracellular_domain
/note= "This sequence is specifically claimed"
1055. .1051
/label= Pepl
/note= "Receptor binding inhibitory peptide. This sequence is specifically claimed"
1064. .1088
/label= Pep2
 /note= "Receptor binding inhibitory peptide. This sequence is specifically claimed"
1095. .1119
/label= Pep5
 note= "Receptor binding inhibitory peptide. This equence is specifically claimed"
 /note= "Receptor binding inhibitory peptide. This sequence is specifically claimed" 1108 /label= Pep4
 /note= "Receptor binding inhibitory peptide. This sequence is specifically claimed"
 Example 1; Page 101-104; 109pp; English.
AAU04591 standard; protein; 1192 AA
 1074. .1098
/label= Pep3
 12-JAN-2000; 2000US-0175707P.
26-MAY-2000; 2000US-0207366P.
29-SEP-2000; 2000US-0236378P.
 12-JAN-2001; 2001WO-US001041
 (first entry)
 WPI; 2001-442138/47.
 Human Nogo protein.
 (UYYA) UNIV YALE.
 N-PSDB; AAS09453
 Strittmatter SM;
 WO200151520-A2
 Homo sapiens.
 26-SEP-2001
 19-JUL-2001
 AAU04591;
 Peptide
 Peptide
 Peptide
 Peptide
 Peptide
 Key
Domain
```

```
Human; Nogo; BACB; acute
stroke; peripheral nerve
 Blackstock WP, Hale RS,
 GLAX) GLAXO GROUP LTD
 WPI; 2002-599722/64.
N-PSDB; ABK90134.
 (first
 protein.
 WO200257483-A2
 sapiens.
 Human NogoA
 21-OCT-2002
 25-JUL-2002.
 196
 250
 1141
 190
 ABG30938;
 172
 172
 Ношо
 12
 ABG3093
 RESULT
 유
 ò
 셤
 8
 8
 ઠે
 g
 ઠ
 셤
 420
injury, stroke or a demyelinating disease selected from multiple sclerosis, monophasis demyelination, encephalomyelitis, multifocal leukoencephalopathy, panencephalitis, Marchiafava-Bignami disease, pontine myelinolysis, adrenoleukodystrophy, Pelizaeus-Merzbacher disease, Spongy degeneration, Alexander's disease, Canavan's disease, metachromatic leukodystrophy, viral infection and Krabbe's disease
 AGLSAAPVPTAPAAGAPLMDFGNDFVPPAPRGPLPAAPPVAPERQPSWDPSPVSSTVPAP 120
 61 AGLSAAPVPTAPAAGAPLMDFGNDFVPPAPRGPLPAAPPVAPERQPSWDPSPVSSTVPAP 120
 171
 121 SPLSAAAVSPSKLPEDDEPPARPPPPPASVSPQAEPVWTPPAPAPAPAPSTPAAPKRRG 180
 171
 SSGSVDETLFALPAASEPVIRSSAENMDLKEQPGNTISAGQEDFPSVLLETAASLPSLSP 240
 171
 241 LSAASFKEHEYLGNLSTVLPTEGTLQENVSEASKEVSEKAKTLLIDRDLTEFSELEYSEM 300
 GSSFSVSPKAESAVIVANPREEIIVKONKDEEEKLVSNNILHNQQELPTALTKLVKEDEVV 360
 171
 171
 480
 171
 540
 171
 600
 171
 601 EESEATPSPVLPDIVMEAPLNSAVPSAGASVIQPSSSPLEASSVNYESIKHEPENPPPYE 660
 661 EAMSVSLKKVSGIKEEIKEPENINAALQETEAPYISIACDLIKETKLSAEPAPDFSDYSE 720
 171
 721 MAKVEQPVPDHSELVEDSSPDSEPVDLFSDDSIPDVPQKQDETVMLVKESLTETSFESMI 780
 171
 840
 171
 841 SNDDLFISKEAQIRETETFSDSSPIEIIDEFPTLISSKTDSFSKLARBYTDLEVSHKSEI 900
 --- 171
 9
 9
 MEDLDQSPLVSSSDSPPRPQPAFKYQFVREPEDEEEEEEEEEDEDEDLEELEVLERKPA
 SSEKAKDSFNEKRVAVEAPMREEYADFKPFERVWEVKDSKEDSDMLAAGGKIESNLESKV
 PLLGDPTSENKTDEKKIEEKKAQIVTEKNTSTKTSNPFLVAAQDSETDYVTTDNLTKVTE
 541 EVVANMPEGLIPDLVQEACESELNEVIGTKIAYETKMDLVQTSEVMQESLYPAAQLCPSF
 781 EYENKEKLSALPPEGGKPYLESFKLSLDNTKDTLLPDEVSTLSKKEKIPLOMEELSTAVY
 MEDLDQSPLVSSSDSPPRPQPAFKYQFVREPEDEEEEEEEEEEDEDLEELEVLERKPA
 421 DKKCFADSLEQTNHEKDSESSNDDTSFPSTPEGIKDRSGAYITCAPFNPAATESIATNIF
 Gaps
 831;
 DB 4; Length 1192,
 SPLSAAAVSPSKLPEDDEPPARPPPPPASVSPQAEPVWTPPAPAPAPPS-
 Indels
 Score 1756.9; DB 4;
Pred. No. 8.5e-61;
0; Mismatches 0;
 95.08;
 30.3%;
 Local Similarity 30.3 es 361, Conservative
 Sequence 1192 AA;
 181
 301
 361
 Query Match
 121
 172
 172
 172
 172
 172
 481
 172
 172
 172
 172
 172
 172
 61
 172
 888888888
 ò
 g
 ઠે
 a
 ò
 원
 a
 ò
 ద
 ઠે
 임
 ò
 g
 ò
 셤
 ઠે
 셤
 ò
 g
 ઠ
 a
 ò
 셤
 Š
 g
 ઠે
 유
 ઠ
 8
 ò
```

```
1020
 1080
 1140
 309
 The present invention relates to a new method of identifying modulators of Nogo function or BACE activity. The method involves providing Nogo and BACE polypeptides capable of binding with each other, monitoring the interaction between these polypeptides, and determining if the test agent is a modulator of Nogo or BACE activity. The method is useful in treating peripheral injuries, such as spinal or head injury, stroke, peripheral nerve damage, and in neoplastic (e.g. glioblastomas, neuroblastomas), hyperproliferative or dysproliferative disorders (e.g. cirrhosis, psoriasis, keloid formation, fibrocystic conditions, tissue hypertrophy) of the central nervous system. The BACE polypeptide is useful in screening methods to identify agents that may act as modulators
 249
 Identifying modulators of Nogo or BACE activity for treating acute neuronal injuries, neoplastic or dysproliferative disorders, comprises providing and monitoring interaction between Nogo and BACE polypeptides.
 Human; Nogo; BACB; acute neuronal injury; spinal injury; head injury; stroke; peripheral nerve damage; neoplastic disorder; glioblastoma: neuroblastoma; hyperproliferative disorder; dysproliferative disorder; cirrhosis; psoriasis; keloid formation; fibrocystic condition; cancer;
 QAEIESIVKPKVLVKEAEKKLPSDTEKEDRSPSAIFSAELSKTSVVDLLYWRDIKKTGVV
 1021 FGASLFLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQAIQKSDEGHPFRAYLESE
 1081 VAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDSLKFAVLMWVFTYVGALFNGLTL
 VAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDSLKFAVLMWVFTYVGALFNGLTL
 FGASLFLLLSLTVFS1VSVTAY1ALALLSVT1SFR1YKGV1QA1QKSDEGHPFRAYLESE
901 ANAPDGAGSLPCTELPHDLSLKNIQPKVEEKISFSDDFSKNGSATSKVLLLPPDVSALAT
 tissue hypertrophy; central nervous system; axon regeneration; NogoA; Nogo-associated disease; metastasis.
 361
 310 LILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAKIPGLKRKAE
 Rowley A;
 Disclosure; Page 59-62; 68pp; English.
 Prinjha R,
 ABG30938 standard; protein; 1192
 SMIK) SMITHKLINE BEECHAM PLC
 18-JAN-2002; 2002WO-GB000228.
 18-JAN-2001; 2001GB-00001312.
 entry)
```

of BACE activity and in particular agents that may be useful in treating Mogo-associated diseases. The modulators of Nogo or BACE polypeptides, and the Polymcleotide encoding the BACE polypeptide are useful in manufacturing a medicament for the treatment or prevention of disorders responsive to the modulation of Nogo activity, in alleviating the gymptoms or improving the condition of a patient suffering from this disorder, in axon regeneration, or in preventing metastasis or spreading of a cancer. The polymucleotide may also be an essential component in assays, a probe, in recombinant protein synthesis, and in gene therapy techniques. The present amino acid sequence represents the human NogoA protein of the invention 888888888888888

Sequence 1192 AA;

AGLSAAPVPTAPAAGAPLMDFGNDFVPPAPRGPLPAAPPVAPERQPSWDPSPVSSTVPAP 120 171 241 LSAASFKEHEYLGNLSTVLPTEGTLQENVSEASKEVSEKAKTLLIDRDLTEFSELEYSEM 300 AGLSAAPVPTAPAAGAPLMDFGNDFVPPAPRGPLPAAPPVAPERQPSWDPSPVSSTVPAP 120 SPLSAAAVSPSKLPEDDEPPARPPPPPASVSPQAEPVWTPPAAPAAPPS----- 171 SSGSVDETLFALPAASEPVIRSSAENMDLKEQPGNTISAGQEDFPSVLLETAASLPSLSP 240 301 GSSFSVSPKAESAVIVANPREEIIVKNKDEEEKLVSNNILHNQQELPTALTKLVKEDEVV 360 --- 171 SSEKAKDSFNEKRVAVEAPMREEYADFKPFERVWEVKDSKEDSDMLAAGGKIESNLESKV 420 421 DKKCFADSLEQTNHEKDSESSNDDTSFPSTPEGIKDRPGAYITCAPFNPAATESIATNIF 480 9 1 MEDLDÓSPLVSSSDSPPRPQPAFKYQFVREPEDEEEEEEEEEEEDEDEDLEELEVLERKPA 0; Indels 831; Gaps Score 1756.9; DB 5; Length 1192; Pred. No. 8.5e-61; 0; Mismatches 95.0%; 30.3%; Matches 361; Conservative Local Similarity 61 19 181 361 172 121 172 172 172 172 Query Match ò g ò d ò ద ò 원 ò g ð g à g ò 유

540

481 PLLGDPTSENKTDEKKIEEKKAQIVTEKNTSTKTSNPFLVAAQDSETDYVTTDNLTKVTE

172

ò g ò g ò q ð g ò 셤 ò a,

172

172

172

172

171

541 EVVANMPEGLTPDLVQEACESELNEVTGTKIAYETKMDLVQTSEVMQESLYPAAQLCPSF 600

171

171

.---- 171

661 EAMSVSLKKVSGIKEEIKEPENINAALQETEAPYISIACDLIKETKLSAEPAPDFSDYSE 720

721 MAKVEQPVPDHSELVEDSSPDSEPVDLFSDDSIPDVPQKQDETVMLVKESLTETSFESMI 780

601 EESEATPSPVLPDIVMEAPLNSAVPSAGASVIQPSSSPLEASSVNYESIKHEPENPPPYE 660

EYENKEKLSALPPEGGKPYLESFKLSLDNTKDTLLPDEVSTLSKKEKIPLQMEELSTAVY 840

781

172

171

| ð  | 172  |                                                                      | 171  |
|----|------|----------------------------------------------------------------------|------|
| QQ | 841  | SNDDLFISKEAQIRETETFSDSSPIBIIDEFPTLISSKTDSFSKLAREYTDLEVSHKSBI         | 006  |
| ò  | 172  |                                                                      | 171  |
| QQ | 901  | ANAPDGAGSLPCTELPHDLSLKNIQPKVEEKISFSDDFSKNGSATSKVLLLPPDVSALAT         | 096  |
| ò  | 172  | V. T. T. T. T. T. T. T. T. T. T. T. T. T.                            | 189  |
| qq | 961  | 961 QAEIESIVKPKVLVKEAEKKLPSDTEKEDRSPSAIFSAELSKTSVVDLLYMRDIKKTGVV     | 1020 |
| ò  | 190  | 190 FGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQAIQKSDEGHPFRAYLESE     | 249  |
| DP | 1021 | FGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQAIQKSDEGHPFRAYLESE         | 1080 |
| ò  | 250  | 250 VAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDSLKFAVLMWVFTYVGALFNGLTL 309 | 309  |
| QΩ | 1081 | VAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDSLKFAVLMMVFTYVGALFNGLTL         | 1140 |
| ò  | 310  | 310 LILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAKIPGLKRKAE 361         |      |
| QQ | 1141 | 1141 LILALISLESVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAKIPGLKRKAE 1192       |      |

Search completed: June 23, 2005, 10:52:04 Job time: 118.158 secs

```
GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
```

OM protein - protein search, using sw model

June 23, 2005, 10:29:31; Search time 25.0347 Seconds (without alignments) 1387.446 Million cell updates/sec Run on:

Title: Perfect score: Sequence:

US-09-830-972-29-FUSED 1850 1 MEDLDQSPLVSSSDSPPRPQ......VKDAMAKIQAKIPGLKRKAE 361

BLOSUM62 Gapop 10.0 , Gapext 0.1 Scoring table:

283416 seqs, 96216763 residues Searched:

283416 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

PIR 79:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

| <b>₹</b> ₹0'*                 |                    | _                  |                    |                    |                    |                    |                    | 6                 |                | <u> </u>           |                    | 6                  |                    | <u>~</u>           |                    | <i>&amp;</i>       |                    | <u></u>            |                    | 6                  |                   | <u></u>            |                    | -<br>-             |                    | <u></u>            |                    | -                  | _                 |   |
|-------------------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|-------------------|----------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|-------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|-------------------|---|
| Description                   | neuroendocrine-spe | neuroendocrine-spe | tropomyosin-relate | hypothetical prote | hypothetical prote | hypothetical prote | C-terminal domain- | formin isoform IV | formin - mouse | cappuccino gene pr | hypothetical prote | probable Pto kinas | unconventional myo | diaphanous protein | unconventional myo | MHC class III hist | unknown protein [i | leukocyte formin p | protein T23E7.2b [ | regulatory protein | DNA topoisomerase | hypothetical prote | probable cell:divi | masquerade precurs | probable transform | hypothetical prote | hypothetical prote | retinoblastoma bin | Bassoon protein - |   |
| ID                            | A46583             | I60904             | A60021             | T26216             | T26215             | T26213             | T31421             | S24407            | S11515         | T13286             | T38236             | F86387             | A59295 ·           | T31065             | A59266             | A35098             | G86441             | JC8033             | D89756             | S54986             | JC6552            | B86369             | G75523             | A55617             | S26058             | T32404             | S48375             | 138902             | T42761            | , |
| DB                            | 2                  | 7                  | ~                  | 7                  | 7                  | 7                  | ~                  | ~                 | ~              | ~                  | ~                  | ~                  | ~                  | ~                  | ~                  | ~                  | ~                  | ~                  | ~                  | N                  | N                 | N                  | N                  | ~                  | ~                  | 7                  | 7                  | П                  | ~                 |   |
| *<br>Query<br>Match Length DB | 776                | 208                | 267                | 2484               | . 2607             | 222                | 1173               | 1206              | 1468           | 1058               | 1611               | 760                | 3511               | 1255               | 3530               | 1132               | 1201               | 1100               | 880                | 980                | 1015              | 731                | 980                | 1047               | 2090               | 1127               | 1375               | 1721               | 3938              |   |
| %<br>Query<br>Match           | 44.7               | 37.0               | 36.0               | 24.6               | 24.2               | 19.1               | 14.9               | 14.4              | 14.4           | 14.3               | 14.2               | 14.1               | 13.9               | 13.9               | 13.8               | 13.7               | 13.7               | 13.6               | 13.5               | 13.5               | 13.4              | 13.4               | 13.4               | 13.4               | 13.4               | 13.2               | 13.2               | 13.2               | 13.2              |   |
| Score                         | 827.7              | 684.2              | 999                | 454.3              | 447                | 353.5              | 275.1              | 266               | 266            | 264.1              | 262.4              | 260.9              | 257.1              | 256.5              | 255.5              | 253.8              | 253.6              | 250.9              | 250.4              | 250                | 247.7             | 247.5              | 247.3              | 247.2              | 247                | 244.8              | 244.8              | 243.6              | 243.4             |   |
| Result<br>No.                 | -                  | 7                  | e                  | 4                  | ß                  | 9                  | 7                  | 8                 | 6              | 10                 | 11                 | 12                 | 13                 | 14                 | 15                 | 16                 | 17                 | 18                 | 19                 | 20                 | 21                | 22                 | 23                 | 24                 | 25                 | 26                 | 27                 | 28                 | 53                |   |

| hypothetical prote |        | hypothetical prote | hypothetical prote | hypothetical prote | progesterone recep | proline-rich prote | progesterone recep | zinc finger protei | BPLF1 protein - hu | T20H2.9 protein - | hypothetical prote | hypothetical prote | 'u     | BNI1 protein - yea | proline-rich prote |
|--------------------|--------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|-------------------|--------------------|--------------------|--------|--------------------|--------------------|
| D96711             | A35466 | E96636             | T26517             | T26998             | QRHUP              | S16748             | A25923             | I84499             | QQBE8              | A86335            | D96728             | T51023             | T49592 | S63244             | S21961             |
| 7                  | ~      | 7                  | N                  | N                  | ч                  | 0                  | ~                  | ~                  | ч                  | ~                 | ~                  | ~                  | ~      | 7                  | ~                  |
| 708                | 786    | 907                | 1634               | 716                | 933                | 449                | 930                | 1706               | 3149               | 1137              | 710                | 2649               | 765    | 1953               | 534                |
|                    |        |                    |                    |                    |                    |                    |                    |                    |                    |                   |                    |                    |        |                    |                    |
|                    | 13.2   | 13.1               | 13.1               | 13.1               | 13.1               | 12.9               | 12.9               | 12.9               | 12.9               | 12.8              | 12.8               | 12.8               | 12.7   | 12.7               | 12.7               |
| 13.2               |        |                    |                    | 242.6 13.1         |                    |                    |                    |                    |                    |                   |                    | 236.7 12.8         |        |                    |                    |

## ALIGNMENTS

|   | RESULT                                                   | 1                                                                                                                                                                  |
|---|----------------------------------------------------------|--------------------------------------------------------------------------------------------------------------------------------------------------------------------|
|   | neuroen<br>N;Conta                                       | neuroendocrine-specific protein, splice form A - human<br>Nyfontains: neuroendocrine-specific protein, splice form B                                               |
|   | C;Speci<br>C;Date:<br>C:Acces                            | C.Date: 24-homo Baptens (man.)<br>C.Date: 24-may-1996 #sequence_revision 24-May-1996 #text_change 09-Jul-2004<br>C.Dacession: A46583: I60903                       |
|   | R, Roebr<br>J. Biol                                      | R. Roebroek, A.J.; van de Velde, H.J.; Van Bokhoven, A.; Broers, J.L.; Ramaekers, F.C.; Ve<br>J. Biol. Chem. 268, 13439-13447, 1993                                |
|   | A;Title:<br>A;Referer                                    | A,Title: Cloning and expression of alternative transcripts of a novel neuroendocrine-spec<br>A,Reference number: A46583; MUID:93293865; PMID:7685762               |
|   | A;Statu<br>A;Statu<br>A;Molec                            | A;Actatus preliminary; translated from GB/EMBL/DDBJ<br>A;Status preliminary; translated from GB/EMBL/DDBJ<br>A;Molecule type: mRNA                                 |
|   | A;Resid<br>A;Cross                                       | A,Residues: 1-776 <rob1><br/>A,Cross-references: UNIPROT:Q16799; GB:L10333; NID:g307306; PIDN:AAA59950.1; PID:g307307<br/>*********************************</rob1> |
|   | A;Acces<br>A;Statu<br>A:Molec                            | A;Accession: louyous<br>A;Status: preliminary; translated from GB/EMBL/DDBJ<br>A:Molecule type: mRNA                                                               |
|   | A; Resid<br>A; Cross                                     | A;Residues: 421-776 <roe2><br/>A;Cross-references: GB:L10334; NID:g307308; PIDN:AAA59951.1; PID:g307309</roe2>                                                     |
| , | C;Genetics:<br>A;Gene: GDB<br>A;Cross-ref<br>A;Map posit | C;Genetics:<br>A;Gene: GDB:RTN1; NSP<br>A;Cross-references: GDB:203968; OMIM:600865<br>A;Map position: 14g21-14g22                                                 |
|   | Query                                                    | Ouery Match 44.7%; Score 827.7; DB 2; Length 776; Best Local Similarity 27.1%; Pred No. 4 Re-20;                                                                   |
|   | Matches                                                  | es 196; Conservative 55; Mismatches 89; Indels 383; Gaps 17;                                                                                                       |
| _ | ò                                                        | 6 QSPL 9                                                                                                                                                           |
|   | q                                                        | :<br>70 QSPVAMETASTGVAGVSSAMDHTFSTTSKDGEGSCYTSLISDICYPPQEDSTYFTGILQK 129                                                                                           |
|   | ò                                                        | 10VSSSDSPRPQP                                                                                                                                                      |
|   | q                                                        |                                                                                                                                                                    |
|   | ò                                                        | 22AFKYQFVREPEDEREREREBEBEDEDELE                                                                                                                                    |
|   | qq                                                       | 190 KAEAYKKIDITRPEEVKHQEQHHPELEDKDLDFKNKDTDISIKPEGVREPDKPAPVEGKI 249                                                                                               |
|   | ò                                                        | 51 53                                                                                                                                                              |
|   | QQ                                                       | 250 IKDHLLEESTFAPYIDDLSEEQRRAPQITTPVKITLTEIEPSVETTTQEKTPEKQDICLK 309                                                                                               |
|   | ò                                                        | 54VLERKPAAGLS 64                                                                                                                                                   |
|   | QQ                                                       | 310 PSPDTVPTVTVSEPEDDSPGSITPPSSGTEPSAAESQGKGSISEDELITAIKBAKGLSYE 369                                                                                               |
|   | λ                                                        | 65AADV PTAPAAGAPL                                                                                                                                                  |
|   |                                                          |                                                                                                                                                                    |

| tropomyosin-related protein, neuronal - rat C;Species: Rattus norvegicus (Norway rat) C;Date: 03-Mar-1993 #sequence_revision 03-Mar-1993 #text_change 05-Nov-1999 C;Accession: A60021 Brain Res. Mol. Brain Res. 10, 33-41, 1991 A;Title: Developmentally regulated cDNA expressed exclusively in neural tissue. Brain Res. Mol. Brain Res. 10, 33-41, 1991 A;Title: Developmentally regulated cDNA expressed exclusively in neural tissue. A;McTecsion: A60021; MUID:91278684; PMID:1647480 A;Accession: A60021; MUID:91278684; PMID:1647480 A;Accession: A60021 A;Molecule type: mRNA A;Residues: 1-367 * vMID. A;Accession: A60021 A;Molecule type: mRNA A;Cross-references: EMBL:X52817; NID:9456549; PIDN:CAA37001.1; PID:9456550 C;Comment: This neuronal-specific mRNA was identified by hybridization to an alpha-tropon Query Match Best Local Similarity 66.1%; Pred. No. 1e-15; Matches 123; Conservative 34; Mismatches 29; Indels 0; Gaps 0; C;Comment: This neuronal-specific mRNA was identified by hybridization to an alpha-tropon Query Match Best Local Similarity 66.1%; Pred. No. 1e-15; Matches 123; Conservative 34; Mismatches 29; Indels 0; Gaps 0; C;Comment: Hill | Qy         352 KIPGLK 357           Db         190 KIPGAR 195           Db         190 KIPGAR 195           RESULT 4         T2616           hypothetical protein W06A7.3c - Caenorhabditis elegans         C;Species: Caenorhabditis elegans           C;Species: Lis-cer-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004           C;Species: Lis-cer-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004           C;Accession: T26216         Ribinated to the EMBL Data Library, August 1996           A;Reference number: Z20173         A;Reference number: Z20173           A;Reference number: Z20174         A;Reference number: Z20173           A;Reference number: Z20173         A;Reference number: Z20173           A;Reference number: Z20174         A;Reference number: Z20174           A;Refer: Z20174         A;Reference number: Z20174           A;Refer: Z20174         A;Reference number: Z20174           A;Refer: Z20174         A;Refer: Z20174           A;Refer: Z20174         A;Refer: Z20174           A;Refer: Z20174                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               |
|----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|-------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| 05   07   TAENPRPVGQLADRAPEVKARSGPPTIPSPLDHEASSAESGDSEIELVSEDPMAAEDA   426   07   07   07   07   07   07   07   0                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            | RESULT 2 160004 100006 100006 100006 100006 100006 100006 100006 100006 100006 100006 100006 100006 100006 100006 100006 100006 100006 100006 100006 100006 100006 100006 100006 100006 100006 100006 100006 100006 100006 100006 100006 100006 100006 100006 100006 100006 100006 100006 100006 100006 100006 100006 100006 100006 100006 100006 100006 100006 100006 100006 100006 100006 100006 100006 100006 100006 100006 100006 100006 100006 100006 100006 100006 100006 100006 100006 100006 100006 100006 100006 100006 100006 100006 100006 100006 100006 100006 100006 100006 100006 100006 100006 100006 100006 100006 100006 100006 100006 100006 100006 100006 100006 100006 100006 100006 100006 100006 100006 100006 100006 100006 100006 100006 100006 100006 100006 100006 100006 100006 100006 100006 100006 100006 100006 100006 100006 100006 100006 100006 100006 100006 100006 100006 100006 100006 100006 100006 100006 100006 100006 100006 100006 100006 100006 100006 100006 100006 100006 100006 100006 100006 100006 100006 100006 100006 100006 100006 100006 100006 100006 100006 100006 100006 100006 100006 100006 100006 100006 100006 100006 100006 100006 100006 100006 100006 100006 100006 100006 100006 100006 100006 100006 100006 100006 100006 100006 100006 100006 100006 100006 100006 100006 100006 100006 100006 100006 100006 100006 100006 100006 100006 100006 100006 100006 100006 100006 100006 100006 100006 100006 100006 100006 100006 100006 100006 100006 100006 100006 100006 100006 100006 100006 100006 100006 100006 100006 100006 100006 100006 100006 100006 100006 100006 100006 100006 100006 100006 100006 100006 100006 100006 100006 100006 100006 100006 100006 100006 100006 100006 100006 100006 100006 100006 100006 100006 100006 100006 100006 100006 100006 100006 100006 100006 100006 100006 100006 100006 100006 100006 100006 100006 100006 100006 100006 100006 100006 100006 100006 100006 100006 100006 100006 100006 100006 100006 100006 100006 100006 100006 100006 100006 100006 100006 100006 100006 100006 100006 100006 100006 100006 |

|                                                                                  | Qy 43 EDEDED 48 | : : <br>DD 1799 NDDDDDGSECLDSIGDLSERTIQRFNTSIDDPSIRRDSFSSISSFGDRQKFRTAIENIRQ 1858 | Qy 49 | Db 1859 DLLPFQSSVSQYLRSSPNPSQQLLVTNLSMDSPSDLSPNAPPVGFENTAQFLEKLQQEDR 1918 | Qy 58 KPAAG | Db 1919 PSAEGSIDSSGFEKVDHEGLDEFAAPPVHDPMQKSVFGSLGSDDMKPGSQDDGFVFIERN 1978 | Qy 69 79 69 79 69 69 69 69 69 69 69 69 69 69 69 69 69 | Db 1979 BANEATLKKNQKMSSHHNDVIEKNYFNDNAPTAALLESPIAEEARKLVQDAVESASEYKK 2038 | Qy 80 89                          | DD 2039 QAVDSGDEIGRELLDNVEQKIEQVKEPIVDSLHKAYDGVGDFVHETVPNAVDDFVREAEK 2098 | Qу         90         RAPLP 106  | 107SWDPSPVSSTVPAPSPLSAAAAVSPSK                         | Db 2159 QTPEEDETTFDRKGPLTIPEEVEKAAAAQNNDLDDFDPLVTSNTGAAFGAAVGAAAAVES 2218 | 133 LPEDDEPPARPPPPBASVSPQAEPV 158                               | Db 2219 LTEEEMFGHQKFETVPRPPTPPKDISDEDVKPSTVNLGPSHHHSHPSSPPHHSILKHHGDA 2278 | Qy 159 WTPPAPAPAPP170                                                                 | Qy 171 170                       | Db 2339 HVKHHRKFRWNEEQATTMSKLGAVGRGLYALIAFIVNIVLRVGLNVALVVGVAVSAHEAY 2398 | 171STSVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVT | Db 2399 KLTKSSGVLRKKEVLDVIÝWŘDAKKSAIVLSLAĽLVÍPVĽAKYPLLTVVTÝSLÍLLAĽGAA 2458 | Qy 221 ISFRIYKGVIQAIQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNCTIKELRRLFL 280                                                                 | QY 281 VDDLVDSLKFAVLMWVFTYVGALFNGLTLLILALISLFSVPVIYERHQAQIDHYLGLANK 340 | Db 2519 VESPLESIKFGLVLMSLTYIASWFSGFTLAILGLIGLIGVFSVPKVYESNOEAIDPHLATISG 2578 | 341 NVKDAMAKIQAKIPGLK 357                     | :: :<br>2579 HLKNVQNIIDEKLPFLR                                                                                | RESULT 6<br>T26213<br>hvnothetical protein W06A7.3b - Caenorhabditis elegans                                   | C;Species: Caenorhabditis elegans<br>C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004<br>C;Accession: T26213 | lbrary, August 1996 | A:Gratus: preliminary; translated from GB/EMBL/DDBJ<br>A:Molecule type: DNA<br>A:Deciding: 1-222 /ull. |
|----------------------------------------------------------------------------------|-----------------|-----------------------------------------------------------------------------------|-------|---------------------------------------------------------------------------|-------------|---------------------------------------------------------------------------|-------------------------------------------------------|---------------------------------------------------------------------------|-----------------------------------|---------------------------------------------------------------------------|----------------------------------|--------------------------------------------------------|---------------------------------------------------------------------------|-----------------------------------------------------------------|----------------------------------------------------------------------------|---------------------------------------------------------------------------------------|----------------------------------|---------------------------------------------------------------------------|-------------------------------------------------------|----------------------------------------------------------------------------|-----------------------------------------------------------------------------------------------------------------------------------------|-------------------------------------------------------------------------|------------------------------------------------------------------------------|-----------------------------------------------|---------------------------------------------------------------------------------------------------------------|----------------------------------------------------------------------------------------------------------------|-----------------------------------------------------------------------------------------------------------------------------------------|---------------------|--------------------------------------------------------------------------------------------------------|
| : : : <br>1859 DLLPFQSSVSQYLRSSPNPSQQLLVTNLSMDSPSDLSPNAPPVGFENTAQFLEKLQQBDR 1918 | 58 KPAAG 68     | 1919 PSAEGSIDSSGFEKVDHEGLDEFAAPPVHDPMQKSVFGSLGSDDMKPGSQDDGFVFIERN 1978            | 69 79 | 1979 EANEATLKKNOKMSSHHNDVIEKNYFNDNAPTAALLESPIAEEARKLVODAVESASEYKK 2038    | 80 89       | 2039 QAVDSGDEIGRELLDNVEQKIEQVKEPIVDSLHKAYDGVGDFVHETVPNAVDDFVREAEK 2098    | 90PRGPLP 106                                          | 2099 QLPESPVPEKIETPEPLVDIHDTVDKVHDEVDNFLRREPTPPFETDDVAPLSDDKPQFGN 2158    | 107SWDPSPVSSTVPAPSPLSAAAVSPSK 132 | 2159 QTPEEDETTFDRKGPLTIPEEVEKAAAAQNNDLDPFDPLVTSNTGAAFGAAVGAAAAVS 2218     | 133 LPEDDPARPPPPPPASVSPQAEPV 158 | WTPPAPAPAPESTSVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIA |                                                                           | LALLSVTISFRIYKGVIQAIQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNCTIK 27 | 2329 LLALGAAAGFRVFKKVEAQIKKTDSEHPFSEILAQDLTLPQEKVHAQADVFVEHATCIAN 2388     | 274 ELRKLFLVDDLVDSLKFAVLMWVFTYVGALFNGLTLLILALISLFSVPVIYERHQAQIDH 333<br>  :      :  : | 334 YLGLANKNVKDAMAKIQAKIPGLK 357 | 2449 HLATISGHLKAVQNIIDEKLPPLR 2472                                        | RESULT 5                                              | 126215<br>hvnothetical protein W0687 3a - Caenorhahditis elegans           | C;Species: Caenorhabditis elegans<br>C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004<br>C;Accession: T26215 | cough, R.<br>ted to the EMBL Data Library, August 1996                  | prence number: Z20173<br>ssion: T26215                                       | us: preliminary; translated from GB/EMBL/DDBJ | idues: 1-2607 <wil> 98-references: UNIPROT:Q23187; EMBL:Z78066; PIDN:CAB01522.2; GSPDB:GN00023; CESP:Wd</wil> | etics:<br>s: CESP:W06A7.3a<br>sobstion: 1827/1: 1866/3: 1963/3: 1990/3: 2262/1: 2289/1: 2412/1: 2462/2: 2586/2 | Q                                                                                                                                       |                     | 1679 VESLERPLTIITQQKPPEKPTEDIGALSPLSPNTLAEYEEVPMMDMQSVPHSPQEKQEEI 1738<br>39 F FFF 42                  |

S. S. S. S. S. S.

| A;Cross-references: UNIPROT:Q23188; EMBL:Z78066; PIDN:CAB01523.1; GSPDB:GN00023; CESP:Wd<br>A;Experimental source: clone W06A7<br>C;Genetics:<br>A;Genetics: Aspense: CESP:W06A7.3b<br>A;Genet: CESP:W06A7.3b          | Qy         92 GPLPAAPPVAPERQPSWDSSPVSS                                                                                                                                                                                                    |
|------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|-------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| A;Introns: 27/1; 77/2; 201/2                                                                                                                                                                                           | τη του συστερομός το που συστερομός το που συστορομός το που συστορομός το που συστορομός το που συστορομός το                                                                                                                            |
| Query Match 19.1%; Score 353.5; DB 2; Length 222; Best Local Similarity 32.2%; Pred. No. 2.6e-05; Matches 65; Conservative 48; Mismatches 84; Indels 5; Gaps 1;                                                        | 116TVPAPSPLS                                                                                                                                                                                                                              |
| Qy 156 EPUWTPPAPAPPSTSUVDLLYWRDIKKTGUVFGASLFLLLSLTVPSIUSUTAYIALA 215                                                                                                                                                   | Db 532 EKRSGDLEKLPAEVPPSGSDRDSRRRGAVFPSIQDLTDHDLFAIKRTITVGRPDKTEFRA 591 Qy 125AAAVSPS                                                                                                                                                     |
| Qy 216 LLSVTISFRIYKGVIQAIQKSDEGHPFRAYLESEVAISEELVQKXSNSALGHVNCTIKEL 275                                                                                                                                                | Db 592 PSPAPAVSPKGEVLYDSEGLSADERGAKGDKDRRRSGAASSSSREKASRRKALDGDRG 651 Qy 132KLPEDDEP                                                                                                                                                      |
| Oy 276 RRLFLVDDLVDSLKFAVLMWVFTYVGALFNGLTLLILALISLFSVPVIYERHQAQIDHYL 335                                                                                                                                                | Db 652 RDRDRSSKKPRTPKDSAPGSGALPKAPPRSGSSSSSSCSSRKVKLQSKVAVLIREGVSS 711 Qy 140 139                                                                                                                                                         |
| Qy 336 GLANKAVKDAMAKIQAKIPGLK 357  : ::                                                                                                                                                                                | 712 TTPAKDSSSSGLGSIGVKFSRDRESRSPFLKPDERSPAEGVKVAPGSTKPKKTKAKAKAG 140                                                                                                                                                                      |
| RESULT 7                                                                                                                                                                                                               | Db 772 AKKAKGTKGKTKRKYRSKGSSTASGGPGSLKKSKADSCSQAASAKGTEETSWSGE 831 Qy 140parpppppaSvspQaEpvwTp161                                                                                                                                         |
| T11421<br>C-terminal domain-binding protein rAl - rat<br>C.Species: Rattus norvecicus (Norway rat)                                                                                                                     | Db 832 ERTTKAPSTPPPRVAPPPPALTPDSGTVDSSCKTPDVSFLAEEASEDTGVRVGAEEEEEE 891                                                                                                                                                                   |
| C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 09-Jul-2004<br>C;Accession: T31421<br>R;Yuryev, A.; Patturajan, M.; Litingtung, Y.; Joshi, R.V.; Gentile, C.; Gebara, M.; Cord                         | QY         162                                                                                                                                                                                                                            |
| Froc. Natl. Acad. Sci. U.S.A. 93, 6975-6980, 1996 A;Title: The C-terminal domain of the largest subunit of RNA polymerase II interacts wit A;Reference number: Z21024; MUID:96293459; PMID:8692929 A;Accession: T31421 | Qy 174 VVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKG 228                                                                                                                                                                        |
| A,Status: preliminary; translated from GB/EMBL/DDBJ A,Molecule type: mRNA A,Residues: 1-1173 < YUR> A,Residues: 1-1173 < YUR> A,SResidues: UNIPROT:063624; EMBL:U49056; NID:g1438531; PID:g1438532; PIDN:AAC526        | Qy 229 VIQAIQKSDEGHPFRAYLESEVAISEELVQKYSNSALGH                                                                                                                                                                                            |
| h 1173;                                                                                                                                                                                                                | Qy 268VNCVNC                                                                                                                                                                                                                              |
| 3 DLDQSPLV                                                                                                                                                                                                             | QY 286 DSLKFAVLAMAVFTYVGALFNGLTLLILALISLFSVPVIYERHQAQIDHYLGLANKAVKDA 345<br>  :       :                                                                                                                                                   |
| 11                                                                                                                                                                                                                     | Qy 346 MAKIQAKI 353  DD 1104 LRKAVHKICHSKSGEINPVKVSNLVRAYVQRYRYFRKHGRKPGDPPGPPRPPKEPGPPDK 1163                                                                                                                                            |
| 27FVREPEDEBEBEBEBD                                                                                                                                                                                                     | Qy 354PGL 356<br>Db 1164 GGPGL 1168                                                                                                                                                                                                       |
|                                                                                                                                                                                                                        |                                                                                                                                                                                                                                           |
| 252 BFFFPQIDGAFGIPPQADSIRAEGAFKKKVFVVGFEABACLEGKVSVEVVIAGGRALFL<br>45EDEDLEELEVLE                                                                                                                                      | CSpecies: Mus musculus (house mouse) C;Date: 19-Reb-1994 #sequence_revision 10-Nov-1995 #text_change 09-Jul-2004 C;Accession: \$24407                                                                                                     |
| DD 292 PPLPPTUPEIEEGEIVQPEEEERVAANSLEKAARERQPFASVAFLASVAARAAFRASAFKA 351 QY 80 DFGNDFV;PPAPPPAP                                                                                                                        | Kjučkson-Grubby, J., Kuo, A.; Leder, F. Genes Dev. G. 29-37, 1992 A;Title: A variant limb deformity transcript expressed in the embryonic mouse limb define A;Reference number: S24407; MUID:92112033; PMID:1339380 A;Molecule type: mRNA |

us-09-830-972-29-fused.rpr

| A;Residues: 1-1206 <jac><br/>A;Cross-references: UNIPROT:Q05859; EMBL:X62379; NID:g51552; PIDN:CAA44244.1; PID:g51553</jac>                      | 737 EEIETLQAQFELKTFHIRGEHALVTARLEEAIENLKQQLEKRREGCEEMRDVCISTDDDC                                                                                                                                                  |
|--------------------------------------------------------------------------------------------------------------------------------------------------|-------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| Query Match Best Local Similarity 17.3%; Pred. No. 1.7; Matches 102; Conservative 40; Mismatches 97; Indels 350; Gaps 24;                        | 59 -PAA                                                                                                                                                                                                           |
| OY 5 DOSPLVSSSDSPRPQPAFKYQFVREPEDEEB                                                                                                             | OY 62GLSAAPVPTAPAAGAPLMDFGNDFVPPAPRGFLPAAPFVAPERQ 105<br>                                                                                                                                                         |
|                                                                                                                                                  | Qy 106 PSWDPSPVSSTVPAPSPLSAAAVSPSKLPEDDEPPARPPPPPASVSPQAEP 157                                                                                                                                                    |
| 59 -PAA                                                                                                                                          | QY 158 VWTPPAPAPAAPPSTSVVDLLYWRDIKKTGVVFGASLF 195                                                                                                                                                                 |
| 571 SPKAFRNVCIQTDRETFLKFCDAESKATRSSQIVPKKLTISLTQLSPSKDSKDIHAPFQT 62GLSAAPVPTAPAAGAPLMDFGNDFVPPAPRGPLPAAPPVAPERQ                                  | Qy 196 LLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQAIQKSDEGHPFRAY 245                                                                                                                                                     |
| 631 REGISSSSQQKISPPAP-PTPPPLPPPLIPPPPPLPPGGPLPPAPPIPP 67 106 PSWDPSPVSSTVPAPSPLSAAAVSPSKLPEDDEPPARPPPPPASVSPQAEP 15                              | Qy 246 LESEVAISEELVQ                                                                                                                                                                                              |
| 680VCPVSPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPP                                                                                                          | Qy 278 -LFLVDDLVDSLKFAVLMMVFTYVGALFNGLTLJILALISLFSVPVIYBRHQAQIDHYLG 336<br>                                                                                                                                       |
| DD 73U FFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFF                                                                                                       | Oy 337 LANKOVKDAMAKIQAKIPGLKRKAE 361                                                                                                                                                                              |
| Db 777                                                                                                                                           |                                                                                                                                                                                                                   |
| Qy 246 LESEVAISEELVQ                                                                                                                             | RESULT 10<br>T13286<br>cappuccino gene protein - fruit fly (Drosophila melanogaster)                                                                                                                              |
| Qy 278 -LFLVDDLVDSLKFAVLMMVFTYVGALFNGLTLLILALISLFSVPVIYERHQAQIDHYLG 336<br>                                                                      | C;Species: Drosophila melanogaster<br>C;Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 09-Jul-2004<br>C;Accession: T122B R<br>R:Emmons, S.: Phan, H.: Callev, J.: Chen, W.: James, B.: Manseau, L. |
| 337 LANKNVKDAMAKIQAKIPGLKRKAB 361                                                                                                                | Genes Dev. 9, 2482-2494, 1995 A;Title: Cappuccino, a Drosophila maternal effect rene required for polarity of the egg a A:Reference number: 217651; MITD:96033799; PMID:7590229                                   |
| DD 883NRAQEDELTKIRKYYETSKEEDLKLLDKPEQFLHELAQIPNFAERAQ 929                                                                                        | A;Accession: T13286<br>A;Status: preliminary; translated from GB/EMBL/DDBJ<br>A;Molecule type: mRNA                                                                                                               |
| RESULT 9 511515 formin - mouse C;Species: Mus musculus (house mouse) C;Species: Alan-1994 Haemience revision 10-Nov-1995 Hext change 09-Jul-2004 | A;Residues: 1-1058 <emm> A;Cross-references: UNIPROT:Q24120; EMBL:U34258; NID:g1061333; PID:g1061334; PIDN:AAC469; C;Genetics: A;Genetics: capu A;Cene:capu</emm>                                                 |
| Vogt, T.F.; Leder, P.                                                                                                                            | Query Match  Query Match  14.3%; Score 264.1; DB 2; Length 1058;  Best Local Similarity 16.1%; Pred. No. 1.4;  Matches 118. Conservative 47.                                                                      |
| ; PMID:2392150                                                                                                                                   | 9 IVSSSISSPRPQPAFKYOFVREPEDEREEREE 9 IVSSSISSPR                                                                                                                                                                   |
| X53599; NID:952877; PIDN:CAA37668.1; 66; DB 2; Length 1468; 6.2.8; 6.2.8;                                                                        |                                                                                                                                                                                                                   |
| S DQSPLVSSSDSPPRBQPAFKYQFVREPEDBEBBEEEE 4                                                                                                        | QY 89 APRGPLPAAPPVAPERQPSWDPSPVSSTVPAPSPLSAAAVSPSKLPEDDEPPAR 142                                                                                                                                                  |
| 42 EEDE                                                                                                                                          | Qy 143 -PPPPPPASVSPQAEPV                                                                                                                                                                                          |

| 63 62 479 PPKDSSSTSTQPTEQSNAQQAPSPKEEERPLPSEPSQNQPAEYRDTPDTPRNIMPLPGLM 538 | 1                                                                          | 539 SADQPIKVTEPSNDADKAIVAEGPNNEEETKGFVIPETQETSEQQVHKTPSPEKQKVLSP 598 66 APV | $\begin{array}{c}  :  & \\  :  & \\ \end{array}$ PPITTNPDKETLASNEAHEAVPQKPSAPQVTRLMAPQDSSSVVTPSPTSLLDPARAVRKV | 73 78                          |                                                                         | IDEDKONEVDPSTSARALPPPGLRFGKVDTLASLAHDDLDDLPDLPRPRTFSPPPLPKTPSG   | 92GP 93<br>779 EFGDNEFMFPKKSNRVRGHOSRPSTGSQLRNVVPVSIVTSGGRPALPDEMASPSSSIGHP 838 | I                                                                                                             | 339 DESEPTABLINGEN INFERIOR OF THE STAFF OF THE STAFF OF THE STAFF OF THE STAFF OF THE STAFF OF THE STAFF OF THE STAFF OF THE STAFF OF THE STAFF OF THE STAFF OF THE STAFF OF THE STAFF OF THE STAFF OF THE STAFF OF THE STAFF OF THE STAFF OF THE STAFF OF THE STAFF OF THE STAFF OF THE STAFF OF THE STAFF OF THE STAFF OF THE STAFF OF THE STAFF OF THE STAFF OF THE STAFF OF THE STAFF OF THE STAFF OF THE STAFF OF THE STAFF OF THE STAFF OF THE STAFF OF THE STAFF OF THE STAFF OF THE STAFF OF THE STAFF OF THE STAFF OF THE STAFF OF THE STAFF OF THE STAFF OF THE STAFF OF THE STAFF OF THE STAFF OF THE STAFF OF THE STAFF OF THE STAFF OF THE STAFF OF THE STAFF OF THE STAFF OF THE STAFF OF THE STAFF OF THE STAFF OF THE STAFF OF THE STAFF OF THE STAFF OF THE STAFF OF THE STAFF OF THE STAFF OF THE STAFF OF THE STAFF OF THE STAFF OF THE STAFF OF THE STAFF OF THE STAFF OF THE STAFF OF THE STAFF OF THE STAFF OF THE STAFF OF THE STAFF OF THE STAFF OF THE STAFF OF THE STAFF OF THE STAFF OF THE STAFF OF THE STAFF OF THE STAFF OF THE STAFF OF THE STAFF OF THE STAFF OF THE STAFF OF THE STAFF OF THE STAFF OF THE STAFF OF THE STAFF OF THE STAFF OF THE STAFF OF THE STAFF OF THE STAFF OF THE STAFF OF THE STAFF OF THE STAFF OF THE STAFF OF THE STAFF OF THE STAFF OF THE STAFF OF THE STAFF OF THE STAFF OF THE STAFF OF THE STAFF OF THE STAFF OF THE STAFF OF THE STAFF OF THE STAFF OF THE STAFF OF THE STAFF OF THE STAFF OF THE STAFF OF THE STAFF OF THE STAFF OF THE STAFF OF THE STAFF OF THE STAFF OF THE STAFF OF THE STAFF OF THE STAFF OF THE STAFF OF THE STAFF OF THE STAFF OF THE STAFF OF THE STAFF OF THE STAFF OF THE STAFF OF THE STAFF OF THE STAFF OF THE STAFF OF THE STAFF OF THE STAFF OF THE STAFF OF THE STAFF OF THE STAFF OF THE STAFF OF THE STAFF OF THE STAFF OF THE STAFF OF THE STAFF OF THE STAFF OF THE STAFF OF THE STAFF OF THE STAFF OF THE STAFF OF THE STAFF OF THE STAFF OF THE STAFF OF THE STAFF OF THE STAFF OF THE STAFF OF THE STAFF OF THE STAFF OF THE STAFF OF THE STAFF OF THE STAFF OF THE STAFF OF THE STAFF OF THE STAFF OF THE STAFF OF | SNVATPPLKQDVTESKASPVADASATHQSSTGLTQEITQLGSNMRLPTKLTRPSNDGRKA | VPAPSPLSAAAVSPSKLPEDDEPPARPVPAPSPLSAAAVSPSKLPEDDEPPARP | 959 SGFKFFAAFFSTFFFFFFSFTSFTSFFFAAFLSKFVSTSFAAFLAKVFFVFFLS 1016 | PS         | 157PVWTPPAPAP                                                                                                                  | 1076 IPAPSGAPPVPAPSGIPPVPKPSVAAPPVPKPSVAVPPVPAPSGAPPVPKPSVAAPPVPV 1135                              | 167 170<br>       <br>1136 PSGAPPVPKPSVAAPPVPAPSGAPPVPKPSVAAPPVPAPSSGIPPVPKPAAGVPPVPPPS 1195                                                           | 171 170                                                                    | 1196 EAPPVPKPSVGVPPVPPPSTAPPVPTPSAGLPPVPVPTAKAPPVPAPSSEAPSVSTPRSS 1255                                                                      | 171 170         | 1256 VPSPHSNASPSPTSSSMASAAPARTSVSRSKSKAERHETSTSSRKSSKSGEHHHHHNEGH 1315 | STSVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYI         | ADSSSTRTSLAHQDSRKSLHRHLSRSSSRASKKPSIVSTTGPFNESFSAKPVE | 213 ALALLSVTISFRIYKGV | IQAIQKSDEGHPFRAYLESEVAISBELVQKYSNSALGHVNCTIKELRR                                | 1429 FHNUNTIQUEQUALAPPAQESKAKLIBESIALICSIII.EKKAKAIQSSMUGUSS 1400<br>278 LFLVDDLVDSIKFAVLAMWVFTVVGALFNGLTLLIIALISLFSVPVIYERHQAQIDHYL 335 |                  | 336GLANKAWKDAMAKIQAKIPGLK 357                                           |
|----------------------------------------------------------------------------|----------------------------------------------------------------------------|-----------------------------------------------------------------------------|---------------------------------------------------------------------------------------------------------------|--------------------------------|-------------------------------------------------------------------------|------------------------------------------------------------------|---------------------------------------------------------------------------------|---------------------------------------------------------------------------------------------------------------|-------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|--------------------------------------------------------------|--------------------------------------------------------|-----------------------------------------------------------------|------------|--------------------------------------------------------------------------------------------------------------------------------|-----------------------------------------------------------------------------------------------------|--------------------------------------------------------------------------------------------------------------------------------------------------------|----------------------------------------------------------------------------|---------------------------------------------------------------------------------------------------------------------------------------------|-----------------|------------------------------------------------------------------------|----------------------------------------------------|-------------------------------------------------------|-----------------------|---------------------------------------------------------------------------------|------------------------------------------------------------------------------------------------------------------------------------------|------------------|-------------------------------------------------------------------------|
| & 8                                                                        | ð í                                                                        | g &                                                                         | 7 A                                                                                                           | & A                            | ð                                                                       | qa .                                                             | 충 음                                                                             | 8 8                                                                                                           | g ò                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           | දු අ                                                         | ठें र                                                  | g a                                                             | <b>3</b> 8 | ò                                                                                                                              | q                                                                                                   | <b>상</b> 음                                                                                                                                             | δ                                                                          | qa                                                                                                                                          | ò               | <b>업</b>                                                               | ò                                                  | 셤                                                     | & A                   | ð i                                                                             | g ò                                                                                                                                      | T QO             | ò                                                                       |
| 161 PPAPWRDIKKTAPAAPPSTSVVDLLYWRDIKKT                                      | Db 607 PPAPRPPSVANSTDSTENSGSSPDEPPAANGADAPPATKEIWTEIEETPLDN 662 Qy 187 190 | Db 663 IDEFTELFSRQAIAPVSKPKELKVKRAKSIKVLDPERSRNVGIIWRSLHVPSSEIEHAIY 722     | Qy 191GASLFLLLSLTVFSIVSV 208  Db 723 HIDTSVVSLEALOHMSNICATEDELORIXEAAGGDIFLDHPROFILDTSILSRASERFISC 782        | 209 TAYIALALISVIISFRIYKGVIQAIQ | Db 783 IVFQAEFEESVTLLFRKLETVSQLSQQLIESEDLKLVFSIILTLGNYMNGGNRQRGQADG 842 | 843 FNLDILGKLKDVKSKESHTTLLHFIVRTYIAQRRKEGVHPLBIRLPIPEPADVERAAQMD | 241                                                                             | Db 903 FEEVQQQIFDLNKKFLGCKRTTAKVLAASRPEIMEPFKSKMEEFVEGADKSMAKLHQS 960 Qy 266 GHVNCTIKELRRLFLVDDLVDSLKFAVL 293 | Db 961LDECRDLFLETMRFYHFSPKACTLTLAQCTPDQFFEYWTNFTNDFKDIWK 1010                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 | 294 MWVFTYVGALFNGLTLILALISLFSVPVIYERHQAQIDHYLGLANKNYKDAMAKIQ | DD 1011FD11SLEWEL                                      | Db 1047 LKERMLMRRSK 1057                                        | RESULT 11  | 138236<br>Hypothetical protein SPAC23A1.17 - fission yeast (Schizosaccharomyces pombe)<br>C.Species: Schizosaccharomyces pombe | C.Percesaion: T38236 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004<br>C.Accesaion: T38236 | R;Murphy, L.; Harris, D.; Wood, V.; Barrell, B.G.; Rajandream, M.A.<br>submitted to the EMBL Data Library, February 1998<br>A;Reference number: Z21780 | A;Accession: T38236<br>A;Status: preliminary; translated from GB/EWBL/DDBJ | A;Wolecule type: DNA<br>A;Residuss: 1-1611 «MUR»<br>A. Cross-reference: INTEDPOT. 042964. EMBT. MICHIS: DIDN.CAMIGO: 1. GEDDB.GNOOMES. EDDB | , 55000 SEC. 20 | A;Gene: SPDB:SPAC23A1.17<br>A:Map position: 1                          | Query Match 14.2%; Score 262.4; DB 2; Length 1611; | Pred. No. 4.6;<br>57; Mismatches 112;                 | 2 EDLDQSPLVSSSDSPRP   | UB 239 EELSNAGKVAKUDDEFVVSNIANSDEFASSORFARFUIDLINKAFSUKLINLIFUKRONAGG 538 QY 20 | Db 359 EISEQEEDEYDDAESDEMHSPYSTHEPESEPEDQDEPSEKDDENKDVEEEGEGEGEGEG 418                                                                   | 50 BELEVLERKPAAG | DD 419 DPEEARKIALKERMARMSGGIGMHVFGLPGLAAFIGRKNILKRIFAKSSEEAKSIINDSS 478 |

| do<br>1                                                 |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                | QY 293 308<br>:                                                                                                                                                                                                                       |
|---------------------------------------------------------|--------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|---------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| RESULT 12<br>F86387 .<br>probable E                     | Pto kinase interactor [imported] - Arabidopsis thaliana                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        | Qy 309LLILALIS 336<br>                                                                                                                                                                                                                |
| C;Species<br>C;Date: 0;<br>C;Accessic                   | . Arabidopsis thaliana (mouse-ear cress)<br>2. Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004<br>2n: F86387                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  | Qy 33.7AMIQAKIPGL 356                                                                                                                                                                                                                 |
| R;Theolog:<br>Chin, C.V                                 | is, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; F.; Hughes, B.; Hulzar, L.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     | ngmrlgeselinsäqqsa                                                                                                                                                                                                                    |
| Nature 400<br>A;Authors<br>C.A.; Li,                    | 8, 816-820, 2000<br>: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.<br>J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali,                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          | Db 734 RRMA 737                                                                                                                                                                                                                       |
| Rizzo, M.,<br>A;Authors<br>ker, M.; V<br>A;Title: S     | <pre>Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H. A;Authores Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W. A;Title: Sequence and analysis of chromosome I of the plant Arabidopsis.</pre>                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     | RESULT 13<br>A59295<br>unconventional myosin-15 - mouse                                                                                                                                                                               |
| A, Reteren(<br>A, Accessic<br>A, Status:<br>A, Molecule | ce number: A86141; MUID:21016719; PMID:11130712<br>preliminary<br>½ type: DNA                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  | C.Species: Mus musculus (house mouse)<br>C;Date: 09-Jun-2000 #sequence_revision 09-Jun-2000 #text_change 09-Jul-2004<br>C;Accesion: 25955<br>R;Liang, Y: Wang, A.; Belyantseva, I.A.; Anderson, D.W.; Probst, F.J.; Barber, T.D.; Mil |
| A,Residue:<br>A,Cross-re<br>C,Genetic:<br>A,Map posi    | <pre>B: 1-760 <sto> eferences: UNIPROT:Q9C660; GB:AE005172; NID:g11079512; PIDN:AAG29223.1; GSPDB:Q 6: ft.ton: 1</sto></pre>                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   | an, T.B.; Fridell, R.A.<br>Genomics 61, 243-258, 1999<br>A.Title: Characterization of the human and mouse unconventional myosin XV genes responsit<br>A.Reference number: A59266; MUID:20021762; PMID:10552926                        |
| Query Ma<br>Best Loc                                    | Query Match  14.1%; Score 260.9; DB 2; Length 760;  Best Local Similarity 15.2%; Pred. No. 0.79;  Marches 119; Conservative 57; Mismarches 127; Indels 481; Gans 27.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           | A;Accession: A59295 A;Status: preliminary; not compared with conceptual translation A;Molecule type: mRNA A;Molecule type: mRNA A;Molecule 1-3511 7:TA                                                                                |
| े हे ह                                                  | SSSDSPPROPARKYOFVREPEDEEEEEEEEEEDEDEDLEELEVLE 5                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |                                                                                                                                                                                                                                       |
| } <i>&amp;</i>                                          | DEVPPAPRGPLPAAPPVAPERQ                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         | A/LLD9 - LEGELCOS: NO. 120.01.<br>A/Map postition: 11:33.9<br>F/1209-1871/Domain: myosin motor domain homology <mmo></mmo>                                                                                                            |
| a &                                                     | 43 REPINGNPPETINTPAQSSPPPETPLSSPPPEPSPPSBLIGPPTITPVSPPPE 97 106 PSWDPSPVSSSPVSS                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                | Query Match 13.9%; Score 257.1; DB 2; Length 3511;<br>Best Local Similarity 9.5%; Pred. No. 50;<br>Matches 136; Conservative 46; Mismatches 113; Indels 1139; Gaps 35;                                                                |
| qq                                                      | ;          <br>PTEAPPPANPVSSPPPESSPPPPPPTEAPPTTPITSPSPPTNPPPPPESPPSL                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           | m                                                                                                                                                                                                                                     |
| දුරු දුරු                                               | 118 PAPSPLS                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    | Db 388 PGMPYVYPEEPAFMYPWVPPPIMSPHNPYAHPMDDIAELEEPEETGEERQSTSFRLPSAA 447 Qy 38EEBEEE 43                                                                                                                                                |
| ò                                                       |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                | <br>                                                                                                                                                                                                                                  |
| 음<br>승<br>음                                             | 218 SPPPPGHPKRREQPPPPGSKRPTPSPPSPSDSKRPVHPSPPSPFEETLPPPKPSPDLFS 277 167AAPPSAAPPSTSVVDLLYWRDIKKTGVVFGASLF 195                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  | Qy         44 DEDEBLEELEVLERKPAAGLSAAPVPTAP                                                                                                                                                                                           |
| ୍ବ                                                      |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                | GNDFVPPAPR                                                                                                                                                                                                                            |
| දු දු                                                   | 196 LLLSLTVFSIVSVTAYIALALLSV                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   | Db 549 GPEFGHPTPRPATSLARFLKKTLSEKKPIPRLRGSQKARGGRPPVREAAYKRFGYKLAGM 608 Ov 102 -PEROPSWDPSPVSSTVPAPSPLSAAAVS 129                                                                                                                      |
| }                                                       | The state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the s |                                                                                                                                                                                                                                       |
| qa                                                      | 381 SALLKTQSSAPLVGNRSSNRTYLSQSEPGGFGQSRELFSYEELVIATNGFSDENLLGEGG 440                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           | Qy 130 129                                                                                                                                                                                                                            |
| දු පු                                                   | 224 - RIYKGVIQAIQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNCT 271  224 - RIYKGVIQAIQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNCT 271  41 FGRYYKGVLEDERVAVKQLKIGGGGGGDREFKAVDTISRVHRNILSMVGYC 493                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             | Db 669 PPFSPTFSRPPRLASFYGSLRQHPPPWAAPAHVPFPPQANWWGFABPPGTSPEVAPDLLA 728 Ov 130                                                                                                                                                        |
| È                                                       | 272 IKBLRRLFLVD 292                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            | DD 729 FPVPRPSFRASRSRRAAYGFPSPSLIGSRRRPHLPSPQPSLRSLPGQGYHSPLGPLSP 788                                                                                                                                                                 |
| Ob                                                      | 494 İSENRELLIYDYVPNNNLYFHLHGTPGLDMATRVKİAAGAARGLAYLHEDCHPRIHRDI 553                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            | Qy 130 129                                                                                                                                                                                                                            |

σ

Page

---YSNSALGHVN--CTIKEL-327 HQAQIDHYLG-----LANKAVK-DAMAKIQAKIPGLKRKAE 361 ----RRLFL-----1048 1108 ò g à RESULT 14
T31065
T31065
T31065
G;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Date: 22-Oct-1999 #sequence\_revision 22-Oct-1999 #text\_change 09-Jul-2004
C;Accession: T31065

R;Watanabe, N.; Madaule, P.; Reid, T.; Ishizaki, T.; Watanabe, G.; Kakizuka, A.; Saito, Serico, 3044-3056, 1997
A;Title: P140mDia, a mammalian homolog of Drosophila diaphanous, is a target protein for A;Reference number: Z20961; MUID:97357293; PMID:9214622
A;Accession: T31065
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-1255 < WAT>
A;Coss-references: UNIPROT:008808; EMBL:U96963; NID:92114472; PID:92114473; PIDN:AAC5328
A;Note: binds to GTP-bound form of Rho and binds to profilin ---RKR 1199 DPKKLSVEEFFMDLHNFRNMFLQAVKENOKRRETEEKMRRAKLAKEKAEKERLEKQQKRE 1167 QIADVERDVQNFPAATDEKDKFVEKMTSFVKDAQEQYNKLRMMHSNMETLYKELGDYFVF 1107 31 ------VDDLVDSLKFAVLMWVFTYVGALFNGLTLLILALISLFSVPVIYER 326 223 525 694 ---PSTSVV---- 175 751 871 SMIQNLIKQMPEPEQLKMLSELKEEYDDLAESEQFGVVMGTVPRLRPRLNAILFKL--- 927 928 QFSEQVENIKPEİVSVTAACEELRKSENFSSLLELTLLVGNYMNAGSRNAGAFGFNİSFL 987 ----ASLFLLLSLT 201 31 81 PGVASIPPPPPLPGATAIPPPPPLPGATAIP-----PPPPLPGGTGIPPPPPLPGSV **EKSEAKATELEKKLDSELTARHELQVEMKKMENDFEQKLQDLQGEKDALDSEKQQITAQK** 752 PKKVYKPEVQLRRPNWSKFVAEDLSQDCFWTKVKEDRFENNELFAKLTLAFSAQTKTSKA 812 KKDQEGGEEKKSVQKKKVKELKVLDSKTAQNLSIFLGSFRMPYQEIKNVILEVNEAVLTE ---RIYKGVIQAI-----QKSDEGHP------FRAYLESEVAISEELVQK-----406 OHLLLVRNDYBARPOYYKLIBECVSOIVLHKNGTDPDFKCRHLQIDIBRLVDOMIDKTKV EDEBEER------EEEEEDEDEDLEELEVLERKPAAGLSAAPVPTAPAAGAPLMDF Gaps 575; Length 1255; Indels ---ERQPSWDPSPVSSTVPAPSPLSAAAVSPSKLPEDDEPPARP--13.9%; Score 256.5; DB 2; 14.7%; Pred. No. 3.9; iive 42; Mismatches 135; -----LYWRDIK-------PPPPPASVSPQAEPVWTPPAPAPAAP----GNDFVPPAPRGPLPA----APPVAP----202 VFS-----IVSVIA-----Query Match 13.9 Best Local Similarity 14.7 Matches 130; Conservative 6 QSPLVSSSDSPPRPQ-24 995 642 872 32 82 582 176 185 187 103

| 152 SPQAEPVWTP                                                     | 169 -PPSTSVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSI 205 1196 GPPSWRNKWHSIRNLPSMRFREQHGEDGVEDMTQLEDLQETTVLSN 1241 206 VSVTAYIALALLSVT-ISFRIYKGVIQAIQKSDEGHPFRAYLESEVAISEEL 256 1242 LKIRFERNLIYTYIGSILVSVNPYQMFGIY |           | LQISPEGLQKAITFKVTETMREKIFTPLTVESAVDARDAIAKVLYALLFSWLITRVNALV  LQISPEGLQKAITFKVTETMREKIFTPLTVESAVDARDAIAKVLYALLFSWLITRVNALV | 333HYLGLANKNV                                                                 | Search completed: June 23, 2005, 10:57:02<br>Job time : 33.0347 secs |                   |
|--------------------------------------------------------------------|----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|-----------|----------------------------------------------------------------------------------------------------------------------------|-------------------------------------------------------------------------------|----------------------------------------------------------------------|-------------------|
| & 8                                                                | 6 6 6 6 6 6 6                                                                                                                                                                                            | 6 6 6 6 6 | 868686                                                                                                                     | 9 de 90                                                                       | Sea<br>Job                                                           |                   |
| Db 1200 GPRQVNRKAGCAVTSLLASELTKDDAMAPGPVKVPKKSE 1238<br>RRSHH.T 15 | 0 · + · · 0 000000 11 10 7 10 7 10                                                                                                                                                                       |           | 42                                                                                                                         | Db   596 RAGGPAVREAAYKRFGYKLAGMDPEKPGTPIVLRRAQPRARSSNDARRPFAPQPAPRTLS 655   C | Qy         81                                                        | 110 PSPVSSTVPAPSP |

This Page Blank (uspto)

```
GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
```

OM protein - protein search, using sw model

June 23, 2005, 10:17:56; Search time 114.158 Seconds (without alignments) 1619.338 Million cell updates/sec Run on:

US-09-830-972-29-FUSED

1850 1 MEDLDQSPLVSSSDSPPRPQ.....VKDAWAKIQAKIPGLKRKAE 361 Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.1 Scoring table:

1612378 seqs, 512079187 residues Searched:

1612378 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

UniProt\_03:\*
1: uniprot\_sprot:\*
2: uniprot\_trembl:\* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## STIMMARTES

|           | Description                | homod  | homo       | homo   | พนธ แ  | Q8bh78 mus musculu | Q8k3g7 mus musculu | Q9jk11 rattus norv | Q8bgm9 mus musculu | Q8k3g8 mus musculu | Q8iua4 homo sapien | น ธกพ  | Q8k290 mus musculu | Q80w95 mus musculu | Q6rss8 gallus gall |        | ene    | _      | Q7pcj7 macaca fasc | Q6jrv2 xenopus lae | Q6jrv0 xenopus lae | Q6jrv1 xenopus lae | Q99p72 mus musculu | Q6ify4 xenopus tro | Q6jrv4 xenopus lae | Q6jrv3 xenopus lae | Q6jrv9 xenopus lae | Q6jrv7 xenopus lae | Q6jrv8 xenopus lae | gallus g | Q6jrw1 xenopus lae | Q6jrw0 xenopus lae |
|-----------|----------------------------|--------|------------|--------|--------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------|--------------------|--------------------|--------------------|--------|--------|--------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|----------|--------------------|--------------------|
| SUMMARIES | ID                         | Q96B16 | RTN4 HUMAN | Q61PNo | QBBHF5 | Q8BH78             | Q8K3G7             | RTN4 RAT           | Q8BGM9             | Q8K3G8             | Q8IUA4             | Q8BGK7 | Q8K290             | Q80W95             | Q6RSS8             | Q7YRW9 | Q6IM70 | Q6IG15 | Q7PCJ7             | Q6JRV2             | Q6JRV0             | Q6JRV1             | RIN4 MOUSE         | Q6IFY4             | Q6JRV4             | -Q6JRV3            | Q6JRV9             | Q6JRV7             | Q6JRV8             | Q7T224   | Q6JRW1             | Q6JRW0             |
|           | DB                         | 7      | -          | ~      | N      | ~                  | ~                  | -                  | ~                  | 7                  | ~                  | ~      | 7                  | ~                  | ~                  | ~      | 7      | ~      | 7                  | 7                  | ~                  | ~                  | -                  | 7                  | 7                  | ~                  | ~                  | ~                  | 7                  | 7        | ~                  | 7                  |
|           | *<br>Query<br>Match Length | 392    | 1192       | 343    | 375    | 356                | 357                | 1163               | 1162               | 1163               | 986                | 1046   | 639                | 578                | 658                | 199    | 199    | 187    | 199                | 1024               | 1043               | 1055               | 199                | 315                | 330                | 311                | 1013               | 1032               | 1044               | 199      | 323                | 304                |
|           | Query<br>Match             | 99.1   | 95.0       | 90.3   | 82.9   | 82.3               |                    | 79.9               | 78.7               | 77.9               | 55.6               | 53.7   | 53.5               | 53.3               | 52.7               | 50.1   | 49.9   | 49.7   | 49.6               | 49.4               | 49.3               | 49.3               | 49.2               | 48.9               | 48.7               | 48.5               | 47.9               | 47.8               | 47.7               | •        | •                  | 47.5               |
|           | Score                      | 1833.9 | 1756.9     | 1669.8 | 1533   | 1523.1             | 1513               | 1478.8             | 1455.3             | 1441.2             | 1028               | 994    | 989.2              | 986.8              | 974.6              | 927    | 923    | 919    | 918                | 914.5              | 912.6              | 912.4              | 911                | 903.8              | 900.5              | 897.2              | 886.4              | 884.5              | •                  | •        | 881.2              | 878.9              |
|           | Result<br>No.              | 1      | 7          | m      | 4      | 5                  | 9                  | 7                  | 80                 | σ                  | 10                 | 11     | 12                 | 13                 | 14                 | 15     | 16     | 17     | 18                 | 19                 | 20                 | 21                 | 22                 | 23                 | 24                 | 25                 | 56                 | 27                 | 28                 | 29       | 30                 | 31                 |

| O6jrw2 xenopus lae O9gm33 macaca fasc O8K0C0 mus musculu O16799 homo sapien O84548 rattus norv O90638 gallus gall O6ify5 xenopus lae O6jrv6 xenopus lae O6jrv3 xenopus lae O6jrv3 xenopus lae O6jrv3 xenopus lae O6jrv3 xenopus lae O6jrv3 xenopus lae |
|--------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| QÉJEWZ Q9GM33 Q9GM33 Q9GM33 Q9EXTO RTN1_HOMAN Q8FK45 RTN1_RAT Q90658 Q6JEVS Q6JEVS Q6JEW4 Q6SJEW4 Q6SJEW6 Q6SJEW6 Q6SJEW6                                                                                                                              |
| ппиниппиппипп                                                                                                                                                                                                                                          |
| 316<br>1796<br>776<br>776<br>770<br>770<br>1193<br>1193<br>1193<br>1199                                                                                                                                                                                |
| 4 4 4 4 4 4 4 4 4 4 4 4 4 4 6 6 6 6 6 6                                                                                                                                                                                                                |
| 873.1<br>867<br>829.8<br>827.7<br>825.8<br>818.1<br>793.3<br>793.3<br>781.7<br>79.7<br>750.9                                                                                                                                                           |
| 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8                                                                                                                                                                                                                  |

## ALIGNMENTS

```
MEDINES-2138257; PubMed=12477932; DOI=10.1073/pnas.242603899;

MEDINES-2138257; PubMed=12477932; DOI=10.1073/pnas.242603899;

Strausberg R.D., Colling F.S., Wagner L., Shenmen C.M., Schuler G.D.,

R. Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

An Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Bronstein M.J., Usdin T.B., Toshiyuki S., Carninol P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Rosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

Rosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

Rosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

Rosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gubbs R.A.,

Rohards S., Worley K.C., Hale S., Garcia A.M., Gabbs R.A.,

Rahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Rahesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Rayaninski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
 Jones S.J., Marra M.A.; mean and initial analysis of more than 15,000 full-length human meanstation and initial analysis of more cDNA sequences ". Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 MEDLINE=22376540; PubMed=12488097; DOI=10.1016/S0022-2836(02)01179-8; Octtle T., Huber C., van der Putten H., Schwab M.E.; Genouic structure and functional characterisation of the promoters of human and mouse nogo/rtn4, i.
 Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
 Van der Putten H.;
Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; BC016165; AAH16165.1; -.
 Strausberg R.;
Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
 v1-νεc-2001 (TrEMBLrel. 19, Last sequence update) 25-OCT-2004 (TrEMBLrel. 28, Last annotation update) Reficulon 4, isoform D (RTN4 isoform B2).
 392 AA.
 01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last seq
25-OCT-2004 (TrEMBLrel. 28, Last ann
 PRT;
 PRELIMINARY;
 Homo sapiens (Human)
 SEQUENCE FROM N.A.
 SEQUENCE FROM N.A.
 SEQUENCE FROM N.A.
 SEQUENCE FROM N.A.
 NCBI_TaxID=9606;
 TISSUE=Kidney;
RESULT 1
 096B16
 DDTTTDDTTTDDTTTDDTTTDDTTTDDTTTDDTTTDDTTTDDTTTDDTTDDTTTDDTTTDDTTTDDTTTDDTTTDDTTDDTTDDTTDD
```

FROM N.A. (ISOFORMS 1; 2 AND 3)

SEQUENCE

```
300
 61 AGLSAAPVPTAPAAGAPLMDFGNDFVPPAPRGPLPAAPPVAPERQPSWDPSPVSSTVPAP 120
 SPLSAAAVSPSKLPEDDEPPARPPPPASVSPQAEPVWTPPAAPAAAPPST---- 172
 181 SSGSVDETLFALPAASEPVIRSSAVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSYT 240
 269
 270 CTIKELRRIFLVDDLVDSLKFAVLMWVFTYVGALFNGLTLLILALISLFSVPVIYERHQA 329
 301 CTIKELRRLFLVDDLVDSLKFAVLMMVPTYVGALFNGLTLLILALISLFSVPVIYERHQA 360
 9
 9
 1 MEDLDQSPLVSSSDSPPRPQPAFKYQFVREPEDEEEEEEEEEEDEDEDLEELEVLERKPA
 1 MEDLDQSPLVSSSDSPPRPQPAFKYQFVREPEDEEEEEEEEEEEEDEDLEELEVLERKPA
 61 AGLSAAPVPTAPAAGAPLMDFGNDFVPPAPRGPLPAAPPVAPERQPSWDPSPVSSTVPAP
 210 AYIALALLSVTISFRIYKGVIQAIQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVN
 [1] — SEQUENCE FROM N.A. (ISOFORMS 1; 2 AND 3).
SEQUENCE FROM N.A. (ISOFORMS 1; 2 AND 3).
BYDINE-20129242; PubMed=10667780; DOI=10.1038/35000287;
Prinjha R., Moore S.E., Vinson M., Blake S., Morrow R., Christie G., Mchalovich D., Simmons D.L., Walsh F.S.;
M.Tahaloticor of neurite outgrowth in humans.";
Nature 403:383-384(2000).
 MEDLINE=2111,696, PubMed=11126160, DOI=10.1038/sj.onc.1203948;
Tagami S., Eguchi Y., Kinoshita M., Takeda M., Tsujimoto Y.;
"A novel protein, RTN-XS, interacts with both Bcl-XL and Bcl-2 on endoplasmic reticulum and reduces their anti-apoptotic activity."; Oncogene 19:5736-5746(2000).
 28-FEB-2003 (Rel. 41, Last sequence update)
25-OCT-2004 (Rel. 45, Last annotation update)
Reticulon 4 (Neurite outgrowth inhibitor) (Nogo protein) (Foocen)
(Neuroendocrine-specific protein) (NSP) (Neuroendocrine specific protein C homolog) (RTN-x) (Reticulon 5) (My043 protein).
 Eukaryoča, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 31;
 RTN4 HUMAN STANDARD; PRT; 1192 AA.
Q9NQC3; Q9462; Q9BXG5; Q9H212; Q9H313; Q9UQ42; Q9Y293; Q9Y2Y7;
 DB 2; Length 392;
 Pred. No. 1.4e-51;
1; Mismatches 0; Indels
 Pfam; PF02453; Reticulon; 1.
PROSITE; PS50845; RETICULON; 1.
SEQUENCE 392 AA; 42274 MW; D7B2AA5E839E58AD CRC64;
 361 QIDHYLGLANKNVKDAMAKIQAKIPGLKRKAE 392
 330 QIDHYLGLANKNVKDAMAKIQAKIPGLKRKAE 361
 EMBL, AY102285, AAM64242.1; --
GO; GO:0005783; C:endoplasmic reticulum; IEA.
InterPro; IPR003388; Reticulon.
 Score 1833.9;
 Name=RTN4; Synonyms=ASY, KIAA0886, NOGO;
 SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
 28-FEB-2003 (Rel. 41, Created)
 EMBL; AY102278; AAM64247.1; -.
 99.18;
 91.8%;
 Best Local Similarity 91.8
Matches 360; Conservative
 Homo sapiens (Human)
 _TaxID=9606
 173
 Query Match
 RTN4 HUMAN
a
 ò
 원
 ò
 엄
 à
 셤
 ò
 ద
 ò
 g
 ð
 셤
 PACOCO ODE DATE OF THE SERVICE OF TH
```

```
Jin W.-L., Ju G., and G., "Developmentally-regulated alternative splicing in a novel Nogo-A.";
 ×
 TISSUE=Brain;
MEDLINE=99156230; PubMed=10048485;
MEDLINE=99156230; PubMed=10048485;
Migase T., Ishikawa K.-I., Suyama M., Kikuno R., Hirosawa M.,
Miyajima N., Tanaka A., Kotani H., Nomura N., Ohara O.;
"Prediction of the coding sequences of unidentified human genes. XII
The complete sequences of 100 new cDNA clones from brain which code
for large proteins in vitro.";
 SEQUENCE FROM N.A. (ISOFORM 3).
Gu J.R., Wan D.F., Zhao X.T., Zhou X.M., Jiang H.Q., Zhang P.P.,
Qin W.X., Huang Y., Qiu X.K., Qian L.F., He L.P., Li H.N., Yu Y.,
 TISSUB=Pituitary;
Song H., Peng Y., Zhou J., Huang Q., Dai M., Mao Y.M., Yu Y., Xu
Luo B., Hu R., Chen J.;
"Human neuroendocrine-specific protein C (NSP) homolog gene.";
Submitted (JUL-1998) to the EMBL/GenBank/DDBJ databases.
 Yu J., Han L.H., ^{\prime} "Novel human cDNA clones with function of inhibiting cancer cell
 MEDLINE=20237542; PubMed=10773680;
Yang J., Yu L., Bi A.D., Zhao S.-Y.;
"Assignment of the human reticulon 4 gene (RTN4) to chromosome
2p14-->2p13 by radiation hybrid mapping.";
Cytogenet. Cell Genet. 88:101-102(2000).
 "Cloning of a member of the reticulon gene family in human."; Submitted (FEB-1999) to the EMBL/GenBank/DDBJ databases.
 Submitted (AUG-1999) to the EMBL/GenBank/DDBJ databases.
 "Isolation of a cell death-inducing gene.";
Submitted (JUN-1998) to the EMBL/GenBank/DDBJ databases
 Submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases
 Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002)
 FROM N.A. (ISOFORMS 2 AND 3)
 SEQUENCE FROM N.A. (ISOFORMS 2 AND 3)
 TISSUE=Placenta, and Skeletal muscle;
Ito T., Schwartz S.M.;
 SEQUENCE FROM N.A. (ISOFORM 3).
 SEQUENCE FROM N.A. (ISOFORM 1).
 FROM N.A. (ISOFORM 4).
 SEQUENCE FROM N.A. (ISOFORM 2).
 and mouse cDNA sequences.
 TISSUE=Fibroblast;
 Yutsudo M.;
 SEQUENCE
 SEQUENCE
 growth.
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration
 MEDLINE=20499367; PubMed=11042152; DOI=10.1101/gr.140200; Zhang Q.-H., Ye M., Wu X.-Y., Ren S.-X., Zhao M., Zhao C.-J., Fu G., Shen Y., Fan H.-Y., Lu G., Zhong M., Xu X.-R., Han Z.-G., Zhang J.-W., Tao J., Huang Q.-H., Zhou J., Hu G.-X., Gu J., Chen S.-J., Chen Z.; Cloning and functional analysis of cDNAs with open reading frames for 300 previously undefined genes expressed in CD34+ hematopoletic genome Res. 10:1546-1560(2000).
 regeneration.";
J. Neurosci. Res. 67:559-565(2002).

-I. Neurosci. Res. 67:559-566(2002).

-I. FUNCTION: Potent neurite outgrowth inhibitor which may also help block the regeneration of the nervous central system in adults.

Isoform 2 reduces the anti-apoptotic activity of Bcl-xl and Bcl-2. This is likely consecutive to their change in subcellular location, from the mitochondria to the endoplasmic reticulum, after binding and sequestration.
-I. SUBCELLULAR LOCATION: Integrat membrane protein. Endoplasmic reticulum reticulum. Anchored to the membrane of the endoplasmic reticulum.
 TISSUE SPECIFICITY: Isoform 1 Is specifically expressed in brain and testis and weakly in heart and skeletal mucale. Isoform 2 is widely expressed excepted accepted accepted several section 3 is expressed brain, skeletal muscle and adipocytes. Isoform 4 is testis-
 Fournier A.E., Grandpre T., Strittmatter S.M.; "Identification of a receptor mediating Nogo-66 inhibition of axonal
 MEDIINE=21888956; PubMed=11891768; DOI=10.1002/jnr.10134;
Ng C.E.L., Tang B.L.;
"Nogos and the Nogo-66 receptor: factors inhibiting CNS neuron
 SIMILARITY: Contains 1 reticulon domain. CAUTION: Ref.11 sequence differs from that shown due to frameshifts in positions 1149 and 1156.
 TISSUE=Brain;
MEDLINE=20129259; PubMed=10667797; DOI=10.1038/35000226;
GrandPre T., Nakamura F., Vartanian T., Strittmatter S.M.;
"Identification of the Nogo inhibitor of axon regeneration
 MEDLINE=21069055; PubMed=11201742; DOI=10.1038/35053072;
 Mao Y.M., Xie, Y., Zheng Z.H.;
Submitted (MAY-1998) to the EMBL/GenBank/DDBJ databases.
 Li J.M.;
to the EMBL/GenBank/DDBJ databases.
 through 2 putative transmembrane domains.

LATERNATIVE PRODUCTS:

Event_Alternative splicing; Named isoforms=4;

Name=1; Synonyms=RTN 4A, Nogo-A, RTN-XL;

IsoId=QNNC3-1; Sequence=Displayed;

Name=2; Synonyms=RTN 4B, Nogo-B, RTN-XS, Foocen-M;

IsoId=QNNC3-2; Sequence=VSP 005655;

Name=3; Synonyms=RTN 4C, Nogo-C, Foocen-S;
 IsoId=09NQC3-3; Sequence=VSP 005652, VSP 005653;
 SEQUENCE OF 482-1192 FROM N.A. (ISOFORM 1/4)
 SEQUENCE OF 186-1192 FROM N.A. (ISOFORM 1)
 IsoId=Q9NQC3-4; Sequence=VSP 005654;
(ISOFORM 3).
 ISSUE=Umbilical cord blood;
 Nature 403:439-444 (2000).
 Nature 409:341-346(2001)
 TISSUE=Testis;
Sha J.H., Zhou Z.M.,
Submitted (JAN-2001)
SEQUENCE FROM N.A.
 protein
 rissum=Brain;
 TISSUE=Brain;
 regeneration
 Reticulon
 FUNCTION
 POPOLOGY
 REVIEW.
 +
```

98

```
modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
 ä
 61 AGLSAAPVPTAPAAGAPLMDFGNDFVPPAPRGPLPAAPPVAPERQPSWDPSFVSSTVPAP 120
 61 AGLSAAPVPTAPAAGAPLMDFGNDFVPPAPRGPLPAAPPVAPERQPSWDPSPVSSTVPAP 120
 171
 241 LSAASFKEHEYLGNLSTVLPTEGTLQENVSEASKEVSEKAKTLLIDRDLTEFSELEYSEM 300
 301 GSSFSVSPKAESAVIVANPREEIIVKNKDEEEKLVSNNII.HNQQELPTALTKLVKEDEVV 360
 361 SSEKAKDSFNEKRVAVEAPMREEYADFKPFERVWEVKDSKEDSDMLAAGGKIESNLESKV 420
 171
 481 PLLGDPTSENKTDEKKIEEKKAQIVTEKNTSTKTSNPFLVAAQDSETDYVTTDNLTKVTE 540
 600
 601 EESEATPSPVLPDIVMEAPLNSAVPSAGASVIQPSSSPLEASSVNYESIKHEPENPPPYE 660
 421 DKKCFADSLEQTNHEKDSESSNDDTSFPSTPEGIKDRSGAYITCAPFNPAATESIATNIF 480
 9
 1 MEDILOGSPLVSSSDSPPRPQPAFKYQFVREPEDEEEEEEEEEEEDEDEDLEELEVLERKPA 60
outstation
veen the Swiss Institute of Bioinformatics and the EMBL outstati
European Bioinformatics Institute. There are no restrictions on
by non-profit institutions as long as its content is in no
 MEDLDQSPLVSSSDSPPRPQPAFKYQFVREPEDEEEEEEEEEEDEDEDLEELEVLERKPA
 121 SPLSAAAVSPSKLPEDDEPPARPPPPASVSPQAEPVWTPPAPAPAPPS-----
 181 SSGSVDETLFALPAASEPVIRSSAENMDLKEQPGNTISAGQEDFPSVLLETAASLPSLSP
 541 EVVANMPEGLTPDLVQEACESELNEVTGTKIAYETKMDLVQTSEVMQESLYPAAQLCPSF
 Indels 831; Gaps
 DB 1; Length 1192;
 ö
 Pred. No. 6e-48;
0; Mismatches
 Score 1756.9;
 BAA74909.2; ALT_INIT.
AAH01035.1; -.
 AJ251383; CAB99248.1; -. AJ251384; CAB99249.1; -.
 95.0%;
30.3%;
 CAB99250.1;
 AAG17976.1;
 AAH07109.1;
 BAB18927.1;
BAB18928.1;
 AAG12176.1
 AAD31021.1
 AAD27783.1
 AAD31022.1
 Query Match 95.0
Best Local Similarity 30.3
Matches 361, Conservative
 AAG12205
 AAG12177
 AAG40878
 BAA83712
 AF148538;
 AB020693;
 BC007109;
 AF077050;
 BC001035;
 AB040462
 AF148537
 AF08790
 172
 172
 172
 172
 between
the Euro
 EMBL;
 EMBL;
EMBL;
 EMBL;
EMBL;
EMBL;
 EMBL;
EMBL;
EMBL;
 EMBL;
EMBL;
EMBL;
 EMBL;
EMBL;
 EMBL;
 EMBL;
 셤
 셤
 셤
 셤
 셤
 셤
 쉽
 á
 유
 8
 g
 Š
 ð
 8
 8
 8
 8
 ð
 Š
 ઠે
 ò
 ઠે
```

7.2

344

ä

61

91

181

241

ద

ઠે

엄 ò g ò ద ઠે a Š g ò 셤 ò 셤 à 음

ò

```
260 YSNSALGHVNCTIKELRRLFLVDDLVDSLKFAVLMWVFTYVGALFNGLTLLILALISLFS 319
 GPLPAAPPVAPERQPSWDPSPVSSTVPAPSPLSAAAVSPSKLPEDDEPPARPPPPASV 121
 200 LIVFSIVSVTAYIALALLSVTISFRIYKGVIQAIQKSDEGHPFRAYLESEVAISEELVQK 259
 GPLPAAPPVAPEROPSWDPSPVSSTVPAPSPLSAAAVSPSKLPEDDEPPARPPPPPASV 151
 152 SPQAEPVWTPPAPAPAPAPPSTS------VVDLLYWRDIKKTGVVFGASLFLLLS 199
 242 YSNSALGHVNCTIKELRRLFLVDDLVDSLKFAVLMMVFTYVGALFNGLTLLILALISLFS 301
 STRAIN=129/SvcJ7, and 129SvcJ7; MEDILINE=22376540; PubMed=1248097; DOI=10.1016/S0022-2836(02)01179-8; OCETILE T., Huber C., van der Putten H., Schwab M.E.; "Genomic structure and functional characterisation of the promoters of
 EDEEEEEEEEEEEEDEDEELEVLERKPAAGLSAAPVPTAPAAGAPLMDFGNDFVPPAPR
 EDEEEEEEEEEEEDEDEDLEELEVLERKPAAGLSAAPVPTAPAAGAPLMDFGNDFVPPAPR
 Gaps
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
 12;
 DB 2; Length 343;
 90.3%; Score 1669.8; DB 2; Length
96.2%; Pred. No. 2.2e-46;
ive 0; Mismatches 1; Indels
 STRAIN=129SvcJ7;
Van der Putten H., Mir A.;
Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
 Strausberg R.;
Submitted (UUN-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; BCO71848; AAH71848.1; -.
GO; GO:0005783; C:endoplasmic reticulum; IEA.
 to the EMBL/GenBank/DDBJ databases.
 320 VPVIYERHQAQIDHYLGLANKNVKDAMAKIQAKIPGLKRKAE 361
 813207C29AB15BA4 CRC64;
 302 VPVIYERHQAQIDHYLGLANKNVKDAMAKIQAKIPGLKRKAE
 Last sequence update)
Last annotation update)
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
 A
 375
 Created)
 PRT;
 human and mouse nogo/rtn4.";
J. Mol. Biol. 325:299-323(2003).
 InterPro; IPR003388; Reticulon. PEGam; PF02453; Reticulon; 1. SEGUENCE 343 AA, 36918 MW; 1.
 (TrEMBLrel. 23, C
(TrEMBLrel. 23, I
(TrEMBLrel. 27, I
 Best Local Similarity 96.2
Matches 329; Conservative
 PRELIMINARY;
 (TrEMBLrel.
 STRAIN=129/SvcJ7;
Van der Putten H.;
Submitted (MAY-2002)
 Mus musculus (Mouse).
 SEQUENCE FROM N.A.
 SEQUENCE FROM N.A.
 SEQUENCE FROM N.A.
 SEQUENCE FROM N.A.
TISSUE=Eye;
 01-MAR-2003 (
01-MAR-2003 (
05-JUL-2004 (
 Name=Rtn4;
 182
 N
 32
 92
 62
 122
 Query Match
 QBBHF5;
 Q8BHF5
 RESULT
 QBBHF5
ઠ
 셤
 ò
 g
 ò
 셤
 ò
 В
 ò
 셤
 ò
 셤
 MEDINE-Eye,

WEDINE-Eye,

MEDINE-Eye,

MEDINE-Eye,

MEDINE-Eye,

MEDINE-Eye,

MEDINE-Eye,

MEDINE-Eye,

MEDINE-Eye,

MILLE Golling F.S., Wagner L., Shenmen C.M., Schuler G.D.,

MILLE MEDINE F.D., Colling F.S., Wagner L., Shenmen C.M., Schuler G.D.,

MILL MEDINE F., Jordan H., Moore T., Max S.I., Wang J., Hashe F.,

MEDINER, M. Marusina K., Farmer A.A., Rubin G.M., Hong L.,

MEDIACHENKO L., Warusina K., Farmer A.A., Rubin G.M., Hong L.,

MEDIACHENKO L., Woldin T.B., Toshiyuki S., Carninci P., Prange C.,

MEDIACHEN M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

MEDIACHEN M.J., Woldin T.B., Toshiyuki S., Abramson R.D., Mullahy S.J.,

MEDIACHEN M.J., Woldin T.B., Toshiyuki S., Abramson R.D., Mullahy S.J.,

MEDIACHEN S., Worley N.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

MILL MEDIACHEN M.J., McKernan M.J., Madan A., Rodrigues S., Sanchez A.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Miting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Miting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Miting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Mathing M., Madan J.W., Green B.D., Dickson M.C.,

Modriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

A Jones S.J., Marra M.A.;

Medinguez A.C., Marial analysis of more than 15,000 full-length human and mouse CDNA sequences.",
 961 QAEIESIVKPKVLVKEAEKKLPSDTEKEDRSPSAIFSAELSKTSVVDLLYWRDIKKTGVV 1020
 1021 FGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIXKGVIQAIQKSDEGHPFRAYLESE 1080
 1081 VAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDSLKFAVLMMVFTYVGALFNGLTL 1140
 840
 249
 309
 780
 900
 960
171
 661 EAMSVSLKKVSGIKEEIKEPENINAALQETEAPYISIACDLIKETKLSAEPAPDFSDYSE 720
 171
 171
 172 ----TSVVDLLYWRDIKKTGVV 189
 721 MAKVEQPVPDHSELVEDSSPDSEPVDLFSDDSIPDVPQKQDETVMLVKESLTETSFESMI
 901 ANAPDGAGSLPCTELPHDLSLKNIQPKVEEKISFSDDFSKNGSATSKVLLLPPDVSALAT
 VAISEBLVOKYSNSALGHVNCTIKELRRLFLVDDLVDSLKFAVLMWVFTYVGALFNGLTL
 781 EYENKEKLSALPPEGGKPYLESFKLSLDNTKDTLLPDEVSTLSKKEKIPLQMEELSTAVY
 841 SNDDLFISKEAQIRETETFSDSSPIEIIDEFPTLISSKTDSFSKLAREYTDLEVSHKSEI
 190 FGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQAIQKSDEGHPFRAYLESE
 1141 LILALISLESVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAKIPGLKRKAE 1192
 310 LILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAKIPGLKRKAE 361
 Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
 Created)
Last sequence update)
Last annotation update)
 Ą
 343
 05-JUL-2004 (TrEMBLrel. 27, 05-JUL-2004 (TrEMBLrel. 27, 05-JUL-2004 (TrEMBLrel. 27,
 PRELIMINARY;
 Homo sapiens (Human)
 172 -----
 SEQUENCE FROM N.A.
 NCBI_TaxID=9606;
 protein.
 05-JUL-2004
05-JUL-2004
 Name=RTN4;
 172
 172
 250
 172
 OCIPNO
 RTN4
 RESULT 3

(061PN0)

DD 05-U

DD 05-U

DD 05-U

DD 05-U

DD 05-U

DD 05-U

DD 05-U

DD 05-U

DD 05-U

DD 05-U

DD 05-U

DD 05-U

DD 05-U

DD 05-U

DD 05-U

DD 05-U

DD 05-U

DD 05-U

DD 05-U

DD 05-U

DD 05-U

DD 05-U

DD 05-U

DD 05-U

DD 05-U

DD 05-U

DD 05-U

DD 05-U

DD 05-U

DD 05-U

DD 05-U

DD 05-U

DD 05-U

DD 05-U

DD 05-U

DD 05-U

DD 05-U

DD 05-U

DD 05-U

DD 05-U

DD 05-U

DD 05-U

DD 05-U

DD 05-U

DD 05-U

DD 05-U

DD 05-U

DD 05-U

DD 05-U

DD 05-U

DD 05-U

DD 05-U

DD 05-U

DD 05-U

DD 05-U

DD 05-U

DD 05-U

DD 05-U

DD 05-U

DD 05-U

DD 05-U

DD 05-U

DD 05-U

DD 05-U

DD 05-U

DD 05-U

DD 05-U

DD 05-U

DD 05-U

DD 05-U

DD 05-U

DD 05-U

DD 05-U

DD 05-U

DD 05-U

DD 05-U

DD 05-U

DD 05-U

DD 05-U

DD 05-U

DD 05-U

DD 05-U

DD 05-U

DD 05-U

DD 05-U

DD 05-U

DD 05-U

DD 05-U

DD 05-U

DD 05-U

DD 05-U

DD 05-U

DD 05-U

DD 05-U

DD 05-U

DD 05-U

DD 05-U

DD 05-U

DD 05-U

DD 05-U

DD 05-U

DD 05-U

DD 05-U

DD 05-U

DD 05-U

DD 05-U

DD 05-U

DD 05-U

DD 05-U

DD 05-U

DD 05-U

DD 05-U

DD 05-U

DD 05-U

DD 05-U

DD 05-U

DD 05-U

DD 05-U

DD 05-U

DD 05-U

DD 05-U

DD 05-U

DD 05-U

DD 05-U

DD 05-U

DD 05-U

DD 05-U

DD 05-U

DD 05-U

DD 05-U

DD 05-U

DD 05-U

DD 05-U

DD 05-U

DD 05-U

DD 05-U

DD 05-U

DD 05-U

DD 05-U

DD 05-U

DD 05-U

DD 05-U

DD 05-U

DD 05-U

DD 05-U

DD 05-U

DD 05-U

DD 05-U

DD 05-U

DD 05-U

DD 05-U

DD 05-U

DD 05-U

DD 05-U

DD 05-U

DD 05-U

DD 05-U

DD 05-U

DD 05-U

DD 05-U

DD 05-U

DD 05-U

DD 05-U

DD 05-U

DD 05-U

DD 05-U

DD 05-U

DD 05-U

DD 05-U

DD 05-U

DD 05-U

DD 05-U

DD 05-U

DD 05-U

DD 05-U

DD 05-U

DD 05-U

DD 05-U

DD 05-U

DD 05-U

DD 05-U

DD 05-U

DD 05-U

DD 05-U

DD 05-U

DD 05-U

DD 05-U

DD 05-U

DD 05-U

DD 05-U

DD 05-U

DD 05-U

DD 05-U

DD 05-U

DD 05-U

DD 05-U

DD 05-U

DD 05-U

DD 05-U

DD 05-U

DD 05-U

DD 05-U

DD 05-U

DD 05-U

DD 05-U

DD 05-U

DD 05-U

DD 05-U

DD 05-U

DD 05-U

DD 05-U

DD 05-U

DD 05-U

DD 05-U

DD 05-U

DD 05-U

DD 05-U

DD 05-U

DD 05-U

DD 05-U

DD 05-U

DD 05-U

DD 05-U

DD 05-U

DD 05-U

D
```

```
SEQUENCE FROM N.A.
 NCBI_TaxID=10090;
 01-OCT-2002 (
01-OCT-2002 (
01-MAR-2004 (
Nogo-B.
 Name=Rtn4;
 289
 SEQUENCE
 08K3G7;
 Q8K3G7
 RESULT 6
 08K3G7
 셤
 ò
 요
 ð
 g
 ઠ
 셤
 ò
 셤
 8
 g
 à
 SO DR READ DR SO D
 338
 60 AAGLSAAPVPTAPAAGAPLMDFGNDFVPPAPRGPLPAAPPVAPERQPSWDPSPVSSTVPA 119
 61 AAGLSAAPVP--PAA-APLLDFSSDSVPPAPRGPLPAAPPTAPERQPSWERSPAAS---A 114
 120 PSPLSAAAVSPSKLPEDDEPPARPPPPASVSPQAEPVWTPPAPA------ 165
 115 PSLPPAAAVLPSKLPEDDEPPAR--PPAPAGASPLAEPAAPPSTPAAPKRRGSGSVDETL 172
 218
 232
 278
 292
 293 FLVDDLVDSLKFAVLMWVFTYVGALFNGLTLLILALISLFSIPVIYERHQAQIDHYLGLA 352
 9
 SEQUENCE FROM N.A.
STRAIN=129/SvcJ7, and 129SvcJ7;
STRAIN=129/SvcJ7, bubmed=12848097; DOI=10.1016/S0022-2836(02)01179-8;
MEDLINE=22376540; Pubmed=12488097; DOI=10.1016/S0022-2836(02)01179-8;
Oertle T., Huber C., van der Putten H., Schwab M.E.;
"Genomic structure and functional characterisation of the promoters of
 1 MEDIDQSSLVSSSADSPPRPPAFKYQFVTEPEDEEDEEDEEDEEDEEDEELEVLERKP
 173 FALPAASEPVIPSSAVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALLLS
 233 VTISFRIYKGVIQAIQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRL
 1 MEDLDQSPLVSSS-DSPPRPQPAFKYQFVREPEDEEEEEEEEEEDEDLEELEVLERKP
 ---PAAP----PSTSVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLS
 VTISFRIYKGVIQAIQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNCTIKELRRL
 Gaps
 Mus musculus (Mouse).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Mus.
NCBI_TaxID=10090;
 30;
 Length 375;
 23; Indels
 Van der Putten H.;
Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
 40300 MW; 23D9EB19BE671AE6 CRC64;
 Last sequence update)
Last annotation update)
 82.9%; Score 1533; DB 2;
82.8%; Pred. No. 7.4e-42;
EMBL; AY102282; AAM73504.1; -.
EMBL; AY102286; AAM73509.1; -.
MGD; MGI:1915835; Rtn4.
GO; GO:0005513; C:endoplasmic reticulum; IDA.
GO; GO:0005515; F:protein binding; IPI.
GO; GO:0001325; P:neurogenesis; IMP.
GO; GO:0001339; P:neurogenesis; IMP.
InterPro; IPR003388; Reticulon.
Pfam; PF02453; Reticulon; I.
 356 AA
 13; Mismatches
 353 NKSVKDAMAKIQAKIPGLKRKAE 375
 NKNVKDAMAKIQAKIPGLKRKAE 361
 Created)
 human and mouse nogo/rtn4.";
J. Mol. Biol. 325:299-323(2003)
 (TrEMBLrel. 23, TrEMBLrel. 23, TrEMBLrel. 27,
 Best Local Similarity 82.8
Matches 317; Conservative
 PRELIMINARY;
 375 AA;
 SEQUENCE FROM N.A.
 [3]
SEQUENCE FROM N.A.
 STRAIN=129/SvcJ7;
 01-MAR-2003
01-MAR-2003
 05-JUL-2004
 Name=Rtn4;
 166
 219
 279
 SEQUENCE
 Query Match
 Q8BH78;
 Q8BH78
 RESULT 5
 셤
 ò
 g
 ઠે
 g
 ð
 셤
 ઠે
 ద
 ઠે
 g
 ò
 g
```

```
61 AAGLSAAPVP--PAA-APLLDFSSDSVPPAPRGPLPAAPPTAPERQPSWERSPAAS---A 114
 115 PSLPPAAAVLPSKLPEDDBPPAR--PPAPAGASPLAE------PAAPPSTPAAPKRR 163
 228
 229 VIQAIQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDSL 288
 283
 KFAVLMWVFTYVGALFNGLTLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAK 348
 284 KFAVLMWVFTYVGALFNGLTLLILALISLFSIPVIYERHQAQIDHYLGLANKSVKDAMAK 343
 60 AAGLSAAPVPTAPAAGAPLMDFGNDFVPPAPRGPLPAAPPVAPERQPSWDPSPVSSTVPA 119
 120 PSPLSAAAVSPSKLPEDDEPPARPPPPASVSPQAEPVWTPPAPAPAAPPSTS----- 173
 9
 174 ----VVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKG
 164 GSGSVVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKG
 1 MEDLDQSPLVSSS-DSPPRPQPAFKYQFVREPEDEEEEEEEEEEEEDEDEDLEELEVLERKP
 Gape
 Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
 29;
 DB 2; Length 356;
Van der Putten H., Mir A.; Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases. EMBL; AV102281; AAM73503.1; -. EMBL; AV102281; AAM73503.1; -. MGD; MGI:1915835; Rtn4. GO; GO:0005783; C:endOplasmic reticulum; IDA. GO; GO:0005581; F:protein binding; IPI. GO; GO:0001525; P:angiogenesis; IMP. GO; GO:0001399; P:neurogenesis; IDA. Interpro; IPR003388; Reticulon. PFam; PF02453; Reticulon; PFMS; Reticulon; PROSITE; PS50845; RETICULON; 1.
 18; Indels
 STRAIN=BALB/C;
Jin W., Li R., Long M., Shen J., Ju G.;
Jin W., Li R., Long M., Shen J., Ju G.;
Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
EMBL, AY114153; AM77069.1;
GO; MGI:1915835; R.Li.
GO; GO:0005783; C:endoplasmic reticulum; IEA.
InterPro; IPR003388; Reticulon.
 PFam, PF02453; Reticulon; 1.
PROSITE; PS50845; RETICULON; 1.
SEQUENCE 357 AA; 38566 MW; 73BB3D17DFDBDF15 CRC64;
 356 AA; 38403 MW; 4366C03BA9630B56 CRC64;
 Last sequence update)
Last annotation update)
 82.3%; Score 1523.1; DB
84.5%; Pred. No. 1.4e-41;
iive 11; Mismatches 18
 357 AA
 Created)
 PRT;
 (TrEMBLrel. 22, C
(TrEMBLrel. 22, L
(TrEMBLrel. 26, I
 344 IQAKIPGLKRKAE 356
 349 IQAKIPGLKRKAE 361
 Query Match
Best Local Similarity 84.5
Matches 315; Conservative
 PRELIMINARY;
 (TrEMBLrel.
(TrEMBLrel.
```

φ

```
AAGLSAAPVPTAPAAGAPLMDFGNDFVPPAPRGPLPAAPPVAPERQPSWDFSPVSSTVPA 119
 227
 GVIQAIQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDS 287
 283
 PSPLSAAAVSPSKLPEDDEPPARPPPPASVSPQAEPVWTPPAPAPAPAPASTS---- 173
 PSLPPAAAVLPSKLPEDDEPPAR--PPAPAGASPLAE-----PAAPPSTPAAPKRR 163
 164 GSGSVVVDLLYMRDIKKTGVVYFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYK 223
 LKFAVLMWVFTYVGALFNGLTLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMA 347
 LKFAVLMWVFTYVGALFNGLTLLILALISLFSIPVIYERHOAQIDHYLGLANKSVKDAMA 343
 59
 9
 SEQUENCE FROM N.A. (ISOFORM 3), AND PARTIAL SEQUENCE.
STRAIN=Sprague-Dawley, TISSUE=Adipocyte;
MEDLINE=99249816; PubMed=10231557; DOI=10.1016/S0167-4889(99)00033-6;
MOTISE N.J., Roses S.A., Neveu J.M., Lane W.S., Lienhard G.E.;
"Cloning and characterization of a 22 kDa protein from rat adipocytes:
a new member of the reticulon family.";
Biochim. Biophys. Acta 1450:68-76(1999).
 1 HELDQSSLVSSSADSPPRPPPAFKYQFVTEPEDEEDEEDEEDEEDEELEEUERKP
 GVIQAIQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRLFLVDDLVDS
 ----VVDLLYWRDIKKTGVV-FGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYK
 1 MEDLDQSPLVSSS-DSPPRPQPAFKYQFVREPEDEEEEEEEEEEEDEDEDLEELEVLERKP
 Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus.
 two
 SEQUENCE FROM N.A. (ISOFORMS 1; 2 AND 3).
MEDLINE=20129258; PubMed=10667796; DOI=10.1038/35000219;
Chen M.S., Huber A.B., Van der Haar M.E., Frank M., Schnell L.,
Spillmann A.A., Christ F., Schwab M.E.;
"Nogo-A is a myelin-associated neurite outgrowth inhibitor and an antigen for monoclonal antibody IN-1.";
 RIN4_RAT STANDARD; PRT; 1163 AA.
QUXII, QUXILO; QSROD9; QGWUE9; QSWUF0;
28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
26-JUL-2004 (Rel. 44, Last annotation update)
Reticulon 4 (Neurite outgrowth inhibitor) (Nogo protein) (Foocen)
(Glut4 vesicle 20 kDa protein).
 SEQUENCE FROM N.A. (ISOFORMS 2 AND 4).
TSTAIN-MINISTEAR KYOUCY, TISSUBE-VASCULAR SMOOTH MUSCle;
ILO T., Schwartz S.M.;
"Cloning of a member of the reticulon gene family in rat: one of
 18; Indels 30;
 Length 357;
 minor splice variants.";
Submitted (FEB-1999) to the EMBL/GenBank/DDBJ databases
 81.8%; Score 1513; DB 2;
84.2%; Pred. No. 2.9e-41;
iive 11; Mismatches 18;
 344 KIQAKIPGLKRKAE 357
 KIQAKIPGLKRKAE 361
 Best Local Similarity 84.2
Matches 315; Conservative
 Name=Rtn4; Synonyms=Nogo;
 antigen for monoclonal a
Nature 403:434-439(2000)
 Rattus norvegicus (Rat)
 Similarity
 NCBI_TaxID=10116;
 348
 120
 115
 174
 228
 288
 284
 9
 224
 Query Match
 FUNCTION
 RTM4_RATT

TATT A RATT

RTM4_RATT

RTM4 RATT

SE - F

DDT 28 - F

DDT 28 - F

DDT 28 - F

DDT 28 - F

DDT 28 - F

DDT 28 - F

DDT 28 - F

DDT 28 - F

COL RATT

COL RATT

COL RATT

COL RATT

RTM 12 - F

RTM 12 - F

RTM 12 - F

RTM 12 - F

RTM 12 - F

RTM 12 - F

RTM 12 - F

RTM 12 - F

RTM 13 - F

RTM 13 - F

RTM 13 - F

RTM 13 - F

RTM 13 - F

RTM 13 - F

RTM 13 - F

RTM 13 - F

RTM 13 - F

RTM 13 - F

RTM 13 - F

RTM 13 - F

RTM 13 - F

RTM 13 - F

RTM 13 - F

RTM 13 - F

RTM 13 - F

RTM 13 - F

RTM 13 - F

RTM 13 - F

RTM 13 - F

RTM 13 - F

RTM 13 - F

RTM 13 - F

RTM 13 - F

RTM 13 - F

RTM 13 - F

RTM 13 - F

RTM 13 - F

RTM 13 - F

RTM 13 - F

RTM 13 - F

RTM 13 - F

RTM 13 - F

RTM 13 - F

RTM 13 - F

RTM 13 - F

RTM 13 - F

RTM 13 - F

RTM 13 - F

RTM 13 - F

RTM 13 - F

RTM 13 - F

RTM 13 - F

RTM 13 - F

RTM 13 - F

RTM 13 - F

RTM 13 - F

RTM 13 - F

RTM 13 - F

RTM 13 - F

RTM 13 - F

RTM 13 - F

RTM 13 - F

RTM 13 - F

RTM 13 - F

RTM 13 - F

RTM 13 - F

RTM 14 - F

RTM 14 - F

RTM 14 - F

RTM 14 - F

RTM 14 - F

RTM 14 - F

RTM 14 - F

RTM 14 - F

RTM 14 - F

RTM 14 - F

RTM 14 - F

RTM 14 - F

RTM 14 - F

RTM 14 - F

RTM 14 - F

RTM 14 - F

RTM 14 - F

RTM 14 - F

RTM 14 - F

RTM 14 - F

RTM 14 - F

RTM 14 - F

RTM 14 - F

RTM 14 - F

RTM 14 - F

RTM 14 - F

RTM 14 - F

RTM 14 - F

RTM 14 - F

RTM 14 - F

RTM 14 - F

RTM 14 - F

RTM 14 - F

RTM 14 - F

RTM 14 - F

RTM 14 - F

RTM 14 - F

RTM 14 - F

RTM 14 - F

RTM 14 - F

RTM 14 - F

RTM 14 - F

RTM 14 - F

RTM 14 - F

RTM 14 - F

RTM 14 - F

RTM 14 - F

RTM 14 - F

RTM 14 - F

RTM 14 - F

RTM 14 - F

RTM 14 - F

RTM 14 - F

RTM 14 - F

RTM 14 - F

RTM 14 - F

RTM 14 - F

RTM 14 - F

RTM 14 - F

RTM 14 - F

RTM 14 - F

RTM 14 - F

RTM 14 - F

RTM 14 - F

RTM 14 - F

RTM 14 - F

RTM 14 - F

RTM 14 - F

RTM 14 - F

RTM 14 - F

RTM 14 - F

RTM 14 - F

RTM 14 - F

RTM 14 - F

RTM 14 - F

RTM 14 - F

RTM 14 - F

RTM 14 - F

RTM 14 - F

RTM 14 - F

RTM 14 - F

RTM 14 - F

RTM 14 - F

RTM 14 - F

RTM 14 - F

RTM 14 - F

RTM 14 - F

RTM 14 - F

RTM 14 -
 d
 g
 g
 à
 엄
 셤
 원
 à
 셤
 Š
 ò
 ò
 ઠે
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this tatement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
 -!- FUNCTION: Potent neurite outgrowth inhibitor which may also help block the regeneration of the nervous central system in adults (By
 R EMBL; AJ242962; CAB71028.1; -.

R EMBL; AJ242962; CAB71029.1; -.

R EMBL; AJ242962; CAB71029.1; -.

R EMBL; AF132046; AAD31019.1; -.

R EMBL; AF132046; AAD31010.1; -.

R GO; GO:0001076; C:integral to endoplasmic reticulum membrane; IDA.

R GO; GO:0005515; F:protein binding, ISS.

R GO; GO:0005515; F:protein binding, ISS.

DR GO; GO:000987; P:negative regulation of anti-apoptosis; ISS.

DR GO; GO:0019987; P:negative regulation of axon extension; ISS.

DR HorsPro; IPR00388; Reticulon.

DR Pfam; PF0453; Reticulon; 1.

DR PROSITE; PS0645; RETICULON; 1.

MALTERNATIVE splicing; Direct protein sequencing;
 Name=13 Synonymes. Occurred. VP203.

Name=43 Synonymes.Nogo-C, VP203.

IsoId=Q9JXIJ-3; Sequence=VSP_005656, VSP_005657;

Name=45 Synonymes.Foocen.M2;

IsoId=Q9JXIJ-1; Sequence=VSP_005659;

TISSUE SPECIFICITY: Isoforms 1, 2 and 3 are present in optic nerve, spinal cord and cerebral cortex. Isoforms 1 and 2 are present in dorsal root ganglion, sciatic nerve and PC12 cells after longer exposure. Isoforms 2 and 3 are detected in kidney, cartilage, skin, lung and spleen. Isoform 3 is expressed at high level in skeletal muscle. In adult animals isoform 1 is expressed sinily in the nervous system.

SIMILARITY: Contains 1 reticulon domain.
 GrandPre T., Li S., Strittmatter S.M.;
"Nogo-66 receptor antagonist peptide promotes axonal regeneration.";
Nature 417:547-551(2002).
 AVLSAELSKTS -> MDGQKKHWKDK (in isoform
 similarity).
SUBUNIT: Binds to RIN4R. Interacts with Bcl-xl and Bcl-2 (By SUBCLIVIAR LOCATION: Integral membrane protein. Anchored to membrane of the endoplasmic reticulum through 2 putative ALTERNATIVE PRODUCTS:
MEDLINE=22033691; PubMed=12037567; DOI=10.1038/417547a;
 /Fridavsp 005657.
Missing (in isoform 2).
/Fridavsp 005658.
Missing (in isoform 4).
/Fridavsp_005659.
 Missing (in isoform 3). /FIId=VSP 005656.
 Cytoplasmic (Potential)
 Cytoplasmic (Potential)
 Event-Alternative splicing; Named isoforms=4; Name=1; Synonyms=Nogo-A, NI-220-250; Isoforms=4, Isoforms=1, Synonyms=Nogo-B, Foocen-Mi. Isoforms=1, Synonyms=Nogo-B, Foocen-Mi. Isoforms=1, Synonyms=Nogo-B, Poocen-Mi. Isoforms=1, Synonyms=Nogo-B, Poocen-Mi. Isoforms=1, Synonyms=Nogo-B, Poocen-Mi.
 Potential.
Lumenal (Potential).
 959500
 Potential.
 Reticulon.
 Poly-Glu.
 Potential
 Poly-Pro
 EMBL, AF051335, AAF01564.1; -.
EMBL, AA242961; CAB71027.1; -.
EMBL, AJ242962; CAB71028.1; -.
EMBL, AJ242963; CAB71029.1; -.
 1010
 145
964
 975
 975
 975
 965
 173
 192
 DOMAIN
TRANSMEM
 DOMAIN
TRANSMEM
DOMAIN
 VARSPLIC
 VARSPLIC
 /ARSPLIC
 /ARSPLIC
 DOMAIN
```

| FT CONFL<br>SQ SEQUE<br>Query Ma<br>Best Loc<br>Matches<br>Qy<br>Db | CONFLICT 1130 1131 Missing (in Ref. 3; AAD31020).  SEQUENCE 1163 AA; 126386 MW; 8CB894B09E94F086 CRC64;  STY MATCH 79.9%; Score 1478.8; DB 1; Length 1163;  St Local Similarity 27.4%; Pred. No. 6.1e-39;  Cohes 320; Conservative 11; Mismatches 25; Indels 812; Gaps 7;  I MEDLOGSPLVSSS-DSPPRPQPARTYOFVREPEDEE EEEEEEEEEDEDELEELEVLERK 58 | 8 6 8 6 8                | 956 TEKEDRSLSAVLSAELSKTSVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIA 1015 214 LALLSVTISPRIYKGVIQAIQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNCTIK 273 1016 LALLSVTISPRIYKGVIQAIQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIK 1075 274 ELRELFLVDDLVDSLKFAVLMWVFTYVGALFNGLTLLILALISLFSVPVIYERHQAQIDH 333 1076 ELRELFLVDDLVDSLKFAVLMWVFTYVGALFNGLTLLILALISLFSVPVIYERHQAQIDH 1135 334 YLGLANKNVKDAMAKIQAKIPGLKRKAE 361 1136 YLGLANKSVKDAMAKIQAKIPGLKRKAE 361 1136 YLGLANKSVKDAMAKIQAKIPGLKRKAE 1163 |
|---------------------------------------------------------------------|----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|--------------------------|---------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| & q                                                                 | 119 APSPLSAAAVSPSKLPEDDEPPARPPPPPASVSPQAEPVWTPPAPA 165                                                                                                                                                                                                                                                                                       | RESULT<br>Q8BGM9<br>ID Q | LT 8<br>M9<br>Q8BGM9 PRELIMINARY; PRT; 1162 AA.                                                                                                                                                                                                                                                                                                                                                                                                                                 |
| & qa                                                                | 166PAA 168<br>   <br>176 LFALPAASEPVIPSSAEKIMDLMEQPGNTVSSGQEDFPSVLLETAASLPSLSFVSFK 235                                                                                                                                                                                                                                                       | A T D D A                | Q8BGM9;<br>01-MAR-2003 (TrEMBLrel. 23, Created)<br>01-MAR-2003 (TrEMBLrel. 23, Last sequence update)<br>05-JUL-2004 (TrEMBLrel. 27, Last annotation update)                                                                                                                                                                                                                                                                                                                     |
| දු පු                                                               | EHGYLGNLSAVSSSEGTIEETLNEASKELPERATNPFVNRDLAEFSELEYSEMGSSFKGS                                                                                                                                                                                                                                                                                 | OC OC OC                 | RTN4;<br>Name=Rtn4;<br>Mus musculus (Mouse).<br>Enkaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;<br>Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.                                                                                                                                                                                                                                                                                         |
| දු දු                                                               | 169 168 296 PKGESAILVENTKEEVIVRSKDKEDLVCSAALHSPQESPVGKEDRVVSPEKTMDIFNEMQ 355                                                                                                                                                                                                                                                                 | N R R                    | NCBI_TaxID=10090;<br>[1]<br>SEQUENCE FROM N.A.                                                                                                                                                                                                                                                                                                                                                                                                                                  |
| දු දු                                                               | 169 168<br>356 MSVVAPVREEYADFKPFEQAWEVKDTYEGSRDVLAARANVESKVDRKCLEDSLEQKSLGK 415                                                                                                                                                                                                                                                              | R R K                    | STRAINEL29/SVGJ', and L29SVGJ'; MEDLINE-22376540; PubMed-12488097; DOI=10.1016/S0022-2836(02)01179-8; OETLD T., Huber C., van der Putten H., Schwab M.E.; "Genomic Structure and functional characterisation of the promoters of                                                                                                                                                                                                                                                |
| Š                                                                   |                                                                                                                                                                                                                                                                                                                                              | T I                      | human and mouse nogo/rtn4.";<br>J. Mol. Biol. 325:299-323(2003).                                                                                                                                                                                                                                                                                                                                                                                                                |
| g &                                                                 | 416 DSEGRNEDASFPSTPEPVKDSSRAYITCASFTSATESTTANTFPLLEDHTSENKTDEKKI 475                                                                                                                                                                                                                                                                         | X X X Z                  | 121<br>SEQUENCE FROM N.A.<br>STRAIN=129/SvcJ7;<br>Van der Dutten H .                                                                                                                                                                                                                                                                                                                                                                                                            |
| 음                                                                   | BERKAQI I TEKTSPKTSNPFLVAVQDSEADYVTTDTLSKVTEAAVSNMPEGLTPDLVQEA                                                                                                                                                                                                                                                                               | RR                       | Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.                                                                                                                                                                                                                                                                                                                                                                                                                        |
| Š                                                                   | 169 168                                                                                                                                                                                                                                                                                                                                      | R R R                    | SEQUENCE FROM N.A.<br>STRAIL195vcJ7;<br>Van der Ditten H. Mir A.                                                                                                                                                                                                                                                                                                                                                                                                                |
| qa a                                                                | CESELNEATGTKIAYETKVDLVQTSEAIQESLYPTAQLCPSFEBAEATPSPVLPDIVMEA                                                                                                                                                                                                                                                                                 | 128                      | Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases. EMBL, XY102284, AAM73566.1;                                                                                                                                                                                                                                                                                                                                                                                            |
| දු දු                                                               | 169                                                                                                                                                                                                                                                                                                                                          | * # # #                  | EMBL; AY102286; AAM/3511.1; MGD; MGI:1915835; Rtn4. GO; GO:00578; C:endoplasmic reticulum; IDA.                                                                                                                                                                                                                                                                                                                                                                                 |
| ò                                                                   |                                                                                                                                                                                                                                                                                                                                              | 3 5 5<br>5 6 6           | GO; GO:0003125; P:procein binding; iFi.<br>GO; GO:000125; P:angiogeneais; IMP.<br>GO; GO:0007399; P:neurogeneais; IDA.                                                                                                                                                                                                                                                                                                                                                          |
| g ጵ                                                                 | 656 EPESFNAAVQETEAPYISIACDLIKETKLSTEPSPDPSNYSEIAKFEKSVPEHAELVEDS 715                                                                                                                                                                                                                                                                         | 888                      |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 |
| q                                                                   | 716 SPESEPVDLFSDDSIPEVPQTQEEAVMLMKESLTEVSETVAQHKEERLSASPQELGKPYL 775                                                                                                                                                                                                                                                                         | o ĉ                      | SEQUENCE IISZ AA; IZGGIZ MW; GSSG9/FBEEII/GIF CKCG4;<br>Oherv March 78 7%: Score 1455 3: DB 2: Length 1162:                                                                                                                                                                                                                                                                                                                                                                     |
| हे ह                                                                |                                                                                                                                                                                                                                                                                                                                              | Z B E                    | Similarity 27.3%; Pred. No. 3.5e-38;<br>9; Conservative 11; Mismatches 23; Indels                                                                                                                                                                                                                                                                                                                                                                                               |
| 3 &                                                                 | 770 BSFQFNDASIANAHSNUTFILIANAHSNUTFILIANAHTISNUULHSSABUTANSTATIONUTHSSABUTANS 933                                                                                                                                                                                                                                                            | 8,1                      | MEDLDQSPLVSSS-DSPPRPQPAFKYQFVRBPEDEREREEBEBDEDEBLEBLEVLERKP                                                                                                                                                                                                                                                                                                                                                                                                                     |
| οp                                                                  | 836 SSPIBIIDEFPTFVSAKDDSPKLAKEYTDLEVSDKSEIANIQSGADSLPCLELPCDLSFK 895                                                                                                                                                                                                                                                                         | 9 8                      | I MEDILOGSELVSSSADSFFKFFFAFKIQFVIEFEDEEDEEDEEDEEDEEDEEDEEDEEDEEDEEDEEDEED                                                                                                                                                                                                                                                                                                                                                                                                       |
| ò                                                                   | 171 170                                                                                                                                                                                                                                                                                                                                      | <b>8</b>                 | 6U AAGLSAARVETARAAGAKLANDIGUNDEVERARGELERAFEVARERGERGERGERGER 113<br>                                                                                                                                                                                                                                                                                                                                                                                                           |
| qq                                                                  | NIYPKDEVHVSDEFSENRSSVSKASISPSNVSALEPQTEMGSIVKSKSLTKEAEKKLPSD                                                                                                                                                                                                                                                                                 | ò                        | PSPLSAAAVSPSKLPEDDEPPARPPPPASVSPQAEPVWTPPAPA                                                                                                                                                                                                                                                                                                                                                                                                                                    |
| ò                                                                   | 171STSWULLYWRDIKKTGWFGASLFLLESLTWSSIVSYTAYIA 213                                                                                                                                                                                                                                                                                             | qa                       |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 |

| AC 08K3GB; DT 01-OCT-2002 (TrEMBLrel. 22, Created) DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update) DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update) DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update) DT 01-MAR-2004 (Mouse) OS Mus musculus (Mouse) OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus. OX NCBI TaxID=10090; DE CONTENTO PROM N N | RC STRAINEBALB/C; RA Jin W., Long M., Li R., Ju G.; RA Jin W., Long M., Li R., Ju G.; RA Jin W., Long M., Li R., Ju G.; RE Submitted (NRT-2002) to the EMBL/GenBank/DDBJ databases.  RE Submitted (NRT-2002) to the EMBL/GenBank/DDBJ databases.  DR REL; AV14152; AAM77068.1;  DR MGD; MGI:1915835; Rtn4.  DR MGD; GO:0005783; Cerdoplasmic reticulum; IEA.  DR InterPro; IPR03388; Reticulon.  DR FRASITE; PS50845; RETICULON; 1.  DR PROSITE; PS50845; RETICULON; 1.  SQ SEQUENCE 1163 AA: 126690 MW; 6B5F362799417EA4 CRC64;  Query Match  T7.9%; Score 1441.2; DB 2; Length 1163;  Best Local Similarity 27.2%; Pred. NO. 18-37;  Matches 318: Conservative 11: Mismarches 24: Indels 818: Gans 9: | MEDLDOSPLVSS-DSPPRPQPAFKXQFVREPEDEREREREBEBEBDEDLERLEVLERKF 59   | 120 PSPLSAAAVSPSKLPEDDEPPARSVSPQAEPVWTPPARA                             | 169                                                                      | QY         169         169         169         169         169         169         169         169         169         169         169         169         169         169         169         169         169         169         169         169         169         169         169         169         169         169         169         169         169         169         169         169         169         169         169         169         169         169         169         169         169         170         170         170         170         170         170         170         170         170         170         170         170         170         170         170         170         170         170         170         170         170         170         170         170         170         170         170         170         170         170         170         170         170         170         170         170         170         170         170         170         170         170         170         170         170         170         170         170         170         170         170         170         170         170         170 |
|-----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|---------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|------------------------------------------------------------------|-------------------------------------------------------------------------|--------------------------------------------------------------------------|----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| QY         166        PAA                                                                                                                                                                                                                                                                                                                                                                                                                                 | 169                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     | 533 VQEACESELNEATGTKIAYETKVDLVQTSEAIQESIYPTAQLCPSFEBAEATPSPVLPDI | 653 BEIKEPESFNAAAQEAEAPYISIACDLIKETKLSTEPSPEFSNYSBIAKFEKSVPDHCEL 71 171 | 773 GKPYLESFQPNLHITKDAASNEIPTLTKKETISLQMEEFNTAIYSNDDLLSSKEDKMKES 832 171 | DD 953 SDTEKEDRSLTAVLSAELNKTISVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSYTAY 1012  QY 212 IALALLSVTISFRIYKGVIQAIQKSDEGHPFRAVLESEVAISEELVQKYSNSALGHVNCT 271  DD 1013 IALALLSVTISFRIYKGVIQAIQKSDEGHPFRAVLESEVAISEELVQKYSNSALGHVNST 1072  QY 272 IKELRRLFLVDDLVDSLKFAVLMWVFTYVGALFNGTLLLILALISLFSFYVIYERHQAQI 331  DD 1073 IKELRRLFLVDDLVDSLKFAVLMWVFTYVGALFNGTTLLILALISLFSIFVIYERHQAQI 1132  QY 332 DHYLGLANKNVKDAMAKIQAKIPGLKRKAE 361  DD 1133 DHYLGLANKNVKDAMAKIQAKIPGLKRKAE 1162  RESULT 9  Q8K3G8  ID Q8K3G8  PRELIMINARY; PRT; 1163 AA.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 |

17;

21

546

491

23

909 113

66

113

999

```
Eukaryota, Metazoa, Chordata,
Mammalia, Eutheria, Rodentia,
NCBI_TaxID=10090;
 ----VLERKPAAGLSAAPVP-
 114 ------
 23,
23,
 Best Local Similarity 39.2
Matches 250; Conservative
 (TrEMBLrel. 2 (TrEMBLrel. 2 (TrEMBLrel. 2
 PRELIMINARY;
 Mus musculus (Mouse).
 100 -VAP-----
 01-MAR-2003
05-JUL-2004
 01-MAR-2003
 Name=Rtn4;
 22
 54
 114
 785
 205
 Query Match
Best Local S
 265
 325
 950
 Q8BGK7
 11
 RESULT
Q8BGK7
 셤
 음
 a
 a
 ઠ
 엄
 ð
 셤
 ઠે
 qq
 g
 ò
 셤
 g
 g
 ઠે
 ઠે
 ઠ
 ઠે
 ò
 ઠે
 8
 953 SDTEKEDRSLTAVLSAELNKTSVVDLLYWRDIKKTGVVYFGASLFLLLSLTVFSIVSVTA 1012
 772
 170
 832
 170
 210
 YIALALLSVTISFRIYKGVIQAIQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNC 270
 TIKELRRLFLVDDLVDSLKFAVLMWVFTYVGALFNGLTLLILALISLFSVPVIYERHQAQ 330
 ETFSDSSPIEIIDEFPTFVSAKDDSPKEYTDLEVSNKSEIANVQSGANSLPCSELPCDLS 892
 MEDLINE=22376540; PubMed=12488097; DOI=10.1016/S0022-2836(02)01179-8; Oertle T., Huber C., van der Putten H., Schwab M.E.; "Genomic structure and functional characterisation of the promoters of
 (RTN4 isoform
 713 VDDSSPESEPVDLFSDDSIPEVPQTQEEAVMLMKESLTEVSETVTQHKHKERLSASPQEV
 773 GKPYLESFQPNLHITKDAASNEIPTLTKKETISLQMEEFNTAIYSNDDLLSSKEDKMKES
 EEIKEPESFNAAAQEAEAPYISIACDLIKETKLSTEPSPGFSNYSEIAKFEKSVPDHCEL
 893 FKNTYPKDEAHVSDEFSKSRSSVSKVPLLLPNVSALESQIEMGNIVKPKVLTKEAEEKLP
 -----STSVVDLLYWRDIKKTGVV-FGASLFLLLSLTVFSIVSVTA
 Homo sapiens (Human).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
 Van der Putten H.;
Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
 SEQUENCE FROM N.A.
TISSUB=Testis;
Oertle T., Schwab M.E.;
Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases
 01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
8NT4 (RIN4 isoform Ab) (RIN4 isoform D) (RIN4 isoform SP) (RIN4 isoform Ab).
 IDHYLGLANKSVKDAMAKIQAKIPGLKRKAB 1163
 IDHYLGLANKNVKDAMAKIQAKIPGLKRKAE 361
 986 AA.
 human and mouse nogo/rtn4.";
J. Mol. Biol. 325:299-323(2003),
 EMBL; AX102285; AAM64244.1; --
EMBL; AX123246; AAM64250.1; --
EMBL; AX123247; AAM64251.1; --
EMBL; AX123248; AAM64252.1; --
EMBL; AX12329; AAM64253.1; --
EMBL; AX123250; AAM64254.1; --
 PRELIMINARY;
 SEQUENCE FROM N.A.
TISSUE=Testis;
 SEQUENCE FROM N.A.
 Q8IUA4;
01-MAR-2003
 271
 331
 1133
 833
 1073
 171
 171
 171
 211
 171
 Q8IUA4
 RESULT 10
481UA
AC Q81UA
AC Q81UA
DT 01-MA
DT 01-MA
DT 01-MA
DT 01-MA
DT 01-MA
DT 05-JU
OC MAMMA
OC MAMMA
OC MAMMA
OC MAMMA
OC MAMMA
OC MAMMA
OC MAMMA
OC MAMMA
OC MAMMA
OC MAMMA
REA OC TISSU
REA OC TISSU
REA OC TISSU
REA OC TISSU
REA OC TISSU
REA OC TISSU
REA OC TISSU
REA OC TISSU
REA OC TISSU
REA OC TISSU
REA OC TISSU
REA OC TISSU
REA OC TISSU
REA OC TISSU
REA OC TISSU
REA OC TISSU
REA OC TISSU
REA OC TISSU
REA OC TISSU
REA OC TISSU
REA OC TISSU
REA OC TISSU
REA OC TISSU
REA OC TISSU
REA OC TISSU
REA OC TISSU
REA SEGUE
DR EMBEL
DR EMBEL
DR EMBEL
DR EMBEL
DR EMBEL
DR EMBEL
DR EMBEL
DR EMBEL
DR EMBEL
DR EMBEL
 g
 ò
 g
 g
 셤
 ద
 셤
 g
셤
 ò
 ò
 ઠે
 δ
 ઠે
 요
 ઠે
 ò
```

```
LCHVNCTIKELRRLFLVDDLVDSLKFAVLMWVFTYVGALFNGLTLLILALISLFSVPVIY 324
 372 DLVQTSEVMQESLYPAAQLCPSFEESEATPSPVLPDIVMEAPLNSAVPSAGASVIQPSSS 431
 667 TLISSKTDSFSKLAREYTDLEVSHKSEIANAPDGAGSLPCTELPHDLSLKNIQPKVEEKI 726
 727 SFSDDFSKNGSATSKVLLLPPDVSALATQAEIESIVKPKVLVKEAEKKLPSDTEKEDR-- 784
 -----TAPAGAPLMDFGNDF 85
 547 IPDVPQKQDETVMLVKESLTETSFESMIEYENKEKLSALPPEGGKPYLESFKLSLDNTKD
 607 TLLPDEVSTLSKKEKIPLQMEELSTAVYSNDDLFISKEAQIRETETFSDSSPIEIIDEFP
 ----SKLPEDDEPPARP
 IVSVTAYIALALLSVTISFRIYKGVIQAIQKSDEGHPFRAYLESEVAISEELVQKYSNSA
 ----APKYQFVR-EPED----EE------EEEEEEEEEDEDBDLEELE----
 492 ACDLIKETK----LSAEPAPDFSDYSEMAKVEQPVPDHSELVEDSSPDS-EPVDLFSDDS
 145 PPPPASVSPQAEPVWTPPAPAPAPPSTSVVDLLYWRDIKKTGVVFGASLFLLLSLTVFS
 SEQUENCE FROM N.A.
STRAIN=129/SvcJ7, and 129SvcJ7;
MEDLINE=22376540; PubMed=12488097; DOI=10.1016/S0022-2836(02)01179-8;
 Gape
 ----ERQPSWDPSPV----
 Craniata; Vertebrata; Euteleostomi;
Sciurognathi; Muridae; Murinae; Mus
 60; Indels 300;
 Length 986;
 986 AA; 108449 MW; 0CDE8F647036415A CRC64;
 Last sequence update)
Last annotation update)
 ERHQAQIDHYLGLANKNVKDAMAKIQAKIPGLKRKAE 361
 DB 2;
 55.6%; Score 1028; DB 2; 39.2%; Pred. No. 1.8e-24; iive 27; Mismatches 60
 3 DLDQS-----PLVSSSDSPPRP----
EMBL; AY123245; AAM64249.1; -.
GO; GO:0005783; C:endoplasmic reticulum; IEA.
InterPro; IPR003388; Reticulon.
Pfam; PF02453; Reticulon; 1.
PG051TE; PS50845; RETICULON; 1.
SEQUENCE 986 AA; 108449 MW; 0CDE8F6470364
 Ş
 Created)
```

264

204

```
LVDDLVDSLKFAVLMMVFTYVGALFNGLTLLILALISLFSIPVIYERHQAQIDHYLGLAN 1024
 DLVQTSEAIQESIYPTAQLCPSFEEAEATPSPVLPDIVMEAPLNSLLPSTGASVAQPSAS 499
 559
 614
 -----GPLPAAPPVAPERQPSW----- 108
 674
 734
 785
 171
 219
 904
 279
 964
 -----DPSPVSSTVPAPSP 122
 ----SKLPED-----DEPPARPPPPP 147
 844
 85
 ------ 2PA-- 22
 23
, Huber C., van der Putten H., Schwab M.E.; structure and functional characterisation of the promoters of
 TISFRIYKGVIQAIQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRLF
 615 IPEVPQTQEEAVMLMKESLTEVSETVTQHKHKERLSASPQEVGKPYLESFQPNLHITKDA
 675 ASNEIPTLTKKETISLQMEEFNTAIYSNDDLLSSKEDKMKESETFSDSSPIEIIDEFPTF
 ------TSVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSV
 LVDDLVDSLKFAVLMWVFTYVGALFNGLTLLILALISLFSVPVIYERHQAQIDHYLGLAN
 -----PKYQFVR-EPEDEBEREEE----EEEDEDEDLEELE-----
 786 -AHVSDEFSKSRSSVSKVPLLLPNVSALESQIEMGNIVKPKVLTKEAEEKLPSDTEKEDR
 TISFRIYKGVIQAIQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNCTIKELRRLF
 735 VŚAKDDŚPKEYTDLEVSNKSEIANVQSGANSLPCŚELPCDLSFKNTYPKDE-----
 53.7%; Score 994; DB 2; Length 1046; 38.6%; Pred. No. 2.6e-23; ive 31; Mismatches 73; Indels 278; Gaps
 148 PASVSPQAEPVWTPPAPAPAPPS-----
 STRAIN=1295vcJ7;
Van der Putten H., Mir A.;
Submitted (NAY-2002) to the EMBL/GenBank/DDBJ databases.
Submitted (NAY-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AY102280; AAM73502.1;
EMBL; AY102280; AAM73507.1;
MGD; MGI:1915835; Rtn4.
GG; GO:0005518; Cendoplasmic reticulum; IDA.
GG; GO:0005518; F:protein binding; IPI.
GG; GO:0001525; P:anglogenesis; IMP.
GG; GO:0001529; P:neurogenesis; IMP.
InterPro; IPR003388; Reticulon.
 Van der Putten H.;
Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
 1046 AA; 114221 MW; 8CE2E2238ED51222 CRC64;
 DLDQS------PLVSSSDSPPRP-----
 VPPAPR------
 KNVKDAMAKIQAKIPGLKRKAE 361
 Pfam; PF02453; Reticulon; 1.
PROSITE; PS50845; RETICULON; 1.
SEQUENCE 1046 AA; 114221 MW;
 human and mouse nogo/rtn4.";
J. Mol. Biol. 325:299-323(2003)
 Matches 240; Conservative
 LSAAAVSP-----
Oertle T., Huber C.,
 Local Similarity
 SEQUENCE FROM N.A.
 FROM N.A.
 STRAIN=129/SvcJ7
 1025
 m
 440
 23
 96
 123
 905
 965
 340
 SEQUENCE
 54
 109
 172
 220
 280
 Query Match
 g
 g
 g
 g
 g
 ò
 ò
 a
 à
 ద
 ò
 ò
 임
 ò
 ò
 셤
 ò
 셤
 ò
 ò
 ò
```

```
STRAIN-EVBN'N, TISSUE-Mammary tumor. C3;

MEDINE-2238257; PubMed=12477932; DOI=10.1073/pnas.242603899;

Strausberg R.L., Felngold E.A., Grouse L.H., Derge J.G.,

Riausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

Altschul S.F., Zeeberg B., Buerow K.H., Schaefer C.F., Bhat N.K.,

Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,

Diatchenko L., Marusina K., Parmer A.A., Rubin G.M., Hong L.,

Blachenko L., Marusina K., Parmer A.A., Rubin G.M., Hong L.,

Stapleton M., Saares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Raha S.S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Yillalon D.K., Muzny D.W., Sodergren B.J., Lu X., Gibbs R.A.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Boutfard G.G.,

A Hakeeley R.W., Touchman J.W., Green B.D., Dickson M.C.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Buterfield Y.S.,

Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,

T. "Generation and initial analysis of more than 15,000 full-length human
 15;
 108
 207
 22
 85
 92
 93 PLEVPSPVSYDGIKLEPENPPPPYEEAMSVALKTSDAKEEIKEPESFNAAAQEAEAPYISI
 ---- DPSPVSSTVPAPSP
 153 ACDLIKETK----LSTEPSPEFSNYSEIAKFEKSVPDHCELVDDSSPES-EPVDLFSDDS
 86 VPPAPR-----GPLPAAPPVAPERQPSW----
 208 IPEVPQTQEEAVMLMKESLTEVSETVTQHKHKERLSASPQEVGKPYLESFQPNLHITKDA
 DLVQTSEAIQESIYPTAQLCPSFEEAEATPSPVLPDIVMEAPLNSLLPSTGASVAQPSAS
 23 -----FKYQFVR-EPEDEEEEEE----EEEDEDEELE----------
 --TAPAAGAPLMDFGNDF
 Gaps
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. TaxID=10090;
 Indels 278;
 Length 639;
 SEQUENCE FROM N.A.
STRAIN=FYB/N; TISSUE=Mammary tumor. C3;
Strausberg W...
Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases.
 INCELLO, ALLONOS DE LOS DEL LOS DE LOS DE LOS DE LOS DE LOS DE LOS DE LOS DE LOS DE LOS DEL LOS DE LOS DELLAS DE LOS DELLAS DE LOS DELLAS DE LOS DELLAS DELL
 Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 Created)
Last sequence update)
Last annotation update)
 53.5%; Score 989.2; DB 2; 38.6%; Pred. No. 1.2e-23; ive 31; Mismatches 73;
 3 DLDQS------PLVSSSDSPPRP-----
 GO; GO:0005783; C:endoplasmic reticulum; IEA.
InterPro; IPR003388; Reticulon.
 639 AA
 PRT;
 ----VLERKPAAGLSAAPVP-
 01-OCT-2002 (TrEMBLrel. 22, 01-OCT-2002 (TrEMBLrel. 22, 01-MAR-2004 (TrEMBLrel. 26,
 EMBL; BC032192; AAH32192.1;
MGD; MGI:1915835; Rtn4.
 and mouse cDNA sequences.
 Query Match
Best Local Similarity 38.6
Matches 240; Conservative
 PRELIMINARY;
 SEQUENCE FROM N.A.
 Rtn4 protein.
 Name=Rtn4;
 33
 54
 109
 Q8K290
RESULT 12
Q8K290
 8 8
 셤
 q
 à
 à
 ð
 셤
 ò
```

330

276

433

```
LSVIISFRIYKGVIQAIQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELR 493
 ----SKLPEDDEPPARPPPPASVSPQAE 156
 RLFLVDDLVDSLKFAVLMWVFTYVGALFNGLTLLILALISLFSVPVIYERHQAQIDHYLG 336
 136
 191 VSEHKELAEKLSPQFGKCDLFSRQVMPDFPGKESEDQTLILNGKSVENIETDEEQERLVD 250
 -- VP 69
 271 DDSPKEYTDLEVSNKSEIANVQSGANSLPCSELPCDLSFKNTYPKDEAHVSDEFSKSRSS
 LSVTISFRIYKGVIQAIQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNCTIKELR
 ------SSDSPPRPQPAFKYQFVREPEDE
 PVWTPPAPAPAPPSTSVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALAL
 EE----EEEEEEDEDDLE-----ELEVLERKPAAGLSAAP-------
 Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 Gaps
 Caltharp S.A., Pira C.U., McNeill D.S., Liwnicz B.H., Oberg K.C.; Submitted (DEC-2003) to the EMBL/GenBank/DDBJ databases. EMBL; AY494005; AAS18427.1; -. GO; GO:0005783; C:endoplasmic reticulum; IEA.
 331 VFKVPLLLPNVSALESQIEMGNIVKPKVLTKEAEEKLPSDTEKEDR-----
 Query Match 52.7%; Score 974.6; DB 2; Length 658; Best Local Similarity 38.2%; Pred. No. 3.8e-23; Matches 229; Conservative 32; Mismatches 84; Indels 254;
 658 AA; 72075 MW; 14B7A000C5E8CDA5 CRC64;
 05-JUL-2004 (TrEMBLrel. 27, Last sequence update) 05-JUL-2004 (TrEMBLrel. 27, Last annotation update) Neurite outgrowth inhibitor NOGO-A (Fragment).
 SWDPSPVSSTVPAPSPLSAAAVSPSKLPED-----
 Z
 658
 LANKNVKDAMAKIQAKIPGLKRKAE 361
 Created)
 PRT;
 InterPro; IPR003388; Reticulon.
 Pfam; PF02453; Reticulon; 1. PROSITE; PS50845; RETICULON; 1.
 (TrEMBLrel. 27, (TrEMBLrel. 27,
 6 QSPLVS------
 PRELIMINARY;
 SEQUENCE FROM N.A.
 NCBI_TaxID=9031;
 _
::
 127 AVSP-
 377
 131
 157
 217
 434
 277
 494
 337
 32
 68
 101
 SEQUENCE
 Gallus
 14
 RESULT
Q6RSS8
 g
 ઠે
 셤
 Š
 g
 õ
 셤
 ò
 g
 ઠે
 셤
 셤
 ઠ
 ద
 ઠે
 g
 g
 ઠે
 ઠે
 ઠે
 210
ASNEIPTLTKKETISLQMEEFNTAIYSNDDLLSSKEDKMKESETFSDSSPIEIIDEFPTF 327
 -----DEPPARPPPPP 147
 171
 | || : : | |:
379 -AHVSDEFSKSRSSVSKVPLLLPNVSALBSQIEMGNIVKPKVLTKEABEKLPSDTEKEDR 437
 438 SLTAVLSAELNKTSVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSV 497
 TISFRIYKGVIQAIQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNCTIKELRRLF 279
 498 TISFRIYKGVIQAIQKSDEGHPPRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRLF 557
 280 LVDDLVDSLKFAVLMWVFTYVGALFNGLTLLILALISLFSVPVIYERHQAQIDHYLGLAN 339
 91 IACDLIKETKLSTEPSPGFSNYSEIAKFEKSVPDHCELVDDSSPESEPVDLFSDDSIPEV 150
 -----DPSPVSSTVPAPSPLSAA 126
 54
 90
 8
 | | | | | : : | | : : | | : : | | SPLEVPSPVSYDGIKLEPEPPPEEAMSVALKTSDAKEEIKEPESFNAAAQGAAEAPYIS
 -----LERKPAAGLS-----AAP----VPTAPAAGAPLMDFUPPA
 151 PQTQEEAVMLMKESLTEVSETVTQHKHKERLSASPQEVGKPYLESFQPNLHITKDAASNE
 ------TSVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALLLSV
 SPLVSSSD-----SPPRPQPAFKYQFVREPEDEEEEEEEEDEDEDLEELEV----
 ------GPLPAAPPVAPERQPSW------
 Gaps
 Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
 Query Match 53.3%; Score 986.8; DB 2; Length 578; Best Local Similarity 41.1%; Pred. No. 1.1e-23; Matches 232; Conservative 21; Mismatches 85; Indels 227;
 SECUENCE FROM N.A.

Tozaki H., Hirata T.;

Tozaki H., Hirata T.;

Submitred (OCT-2011) to the EMBL/GenBank/DDBJ databases.

EMBL; AB073-672; BAC75974.1; -.

GO; GO:0005783; C:endoplasmic reticulum; IEA.

InterPro; IPR003388; Reticulon.

Pfam; PF03453; Reticulon; 1.

PROSITE; PS50845; RETICULON; 1.
 SEQUENCE 578 AA; 63696 MW; 832670C171E4AC61 CRC64;
 Created)
Last sequence update)
Last annotation update)
 578 AA.
 148 PASVSPQAEPVWTPPAPAPAAPPS-----
 340 KNVKDAMAKIQAKIPGLKRKAE 361
 LSAAAVSP-----
 90 PR-----
 01-JUN-2003 (TrEMBLrel. 24, 01-JUN-2003 (TrEMBLrel. 24, 01-OCT-2003 (TrEMBLrel. 25,
 PRELIMINARY;
 Nogo-A (Fragment).
 NCBI_TaxID=10090;
 Name=Nogo-A;
 172
 220
 618
 31
 22
 109
 TER
 Q80W95
 RESULT 13
080095
AC Q80099
AC Q8009
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT
 유
 ઠે
 g
 8
 셤
 ઠે
 g
 ઠે
 g
 ò
 g
 δ
 셤
 요
 ò
 a
 ò
 셤
 ò
 셤
```

34

ઠે

```
Job time : 119.158 secs
 242
 480 IKKTGVVFGASLFLLLSLTVFSIVSVTAXIALALLSVTISFRIYKGVIQAIQKSDEGHPF 539
 233
 132 MWVFTYVGALFNGLTLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAKI 191
310 AMEPKPGDSKGLSPS-----SPVSVEDDFVMLVDPKTGTEFVAEVTDRETVHKNESKD 362
 -----PQAEPVWTPPAP 164
 165 APAAPPS-----TSVVDLLYWRD 182
 420 ATGTSPSSTEKEIVSVGKPEAFEKEAERGAASAKEKEKPTAVFSAKLNVSSVVDLLYWRD 479
 RAYLESEVAISEELVQKYSNSALGHVNCTIKELRRIFLVDDLVDSLKFAVLMWVFTYVGA 302
 QKSDEGHPFRAYLESEVÄISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDSLKFAVL 293
 MWVFTYVGALFNGLTLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAKI 353
 12 VVDLLYWRDIKKTGVVFGASLFLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQAI 71
 LFNGLTLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAKIPGLKRKAE 361
 363 ISNEIRDEKRQAPLTELPCDLSVRNVEVKTEDDAHALKKSLQAIDREVPEVSMV---SLP
 IKKTGVVFGASLFLLLSLTVFSIVSVTAYIALLLSVTISFRIYKGVIQAIQKSDEGHPF
 174 VVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQAI
 Gaps
 MEDLINE=2715887; PubMed=12832288;
MEDLINE=2715887; PubMed=12832288;
Oertle T., Klinger M., Stuermer C.A., Schwab M.E.;
Oertle T., Klinger M., Stuermer C.A., Schwab M.E.;
Areticular rhapsody: phylogenic evolution and nomenclature of the RIN/Nogo gene family.";
FASEB J. 17:1238-1247(2003).
FASEB J. 17:1238-1247(2003).
GO. GO.0005783; C.endoplasmic reticulum; IEA.
InterPro; IPR003188; Reticulon.
 Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Cetartiodactyla, Ruminantia, Pecora, Bovidae,
Bovinae, Bos.
 ö
 50.1%; Score 927; DB 2; Length 199; ilarity 100.0%; Pred. No. 8e-23; Conservative 0; Mismatches 0; Indels
 Pfam; PF02453; Reticulon; 1.
PROSITE; PS50845; RETICULON; 1.
SEQUENCE 199 AA; 22395 MW; C60161DF3FB34D80 CRC64;
 Last sequence update)
Last annotation update)
 199 AA
 Created)
 -----DEPPARPPPPPASVS--
 Q7YRW9;
01-OCT-2003 (TrEMBLrel. 25,
01-MAR-2004 (TrEMBLrel. 26,
01-MAR-2004 (TrEMBLrel. 26,
 PRELIMINARY;
 PGLKRKAE 361
 |||||||||
PGLKRKAE 199
 RTN4-C.
Name=RTN4;
Bos taurus (Bovine).
 Query Match
Best Local Similarity
Matches 188; Conserv
 Bovinae, Bos.
NCBI_TaxID=9913;
 137
 243
 303
 234
 294
 183
 009
 354
 Q7YRW9
 원
 g
 δ
 à
 셤
 ઠે
 원
 g
 ઠે
 염
 ò
 셤
 셤
 ò
 ò
 ò
 ò
```

Search completed: June 23, 2005, 10:55:59